



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 186418

TO: Minh-Tam Davis
Location: rem/3A24/3C18
Art Unit: 1642
Wednesday, April 26, 2006
Case Serial Number: 09/762577

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: (571)272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Davis,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2523

THIS PAGE BLANK (USPTO)

73622

186416

Mg

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Thursday, April 20, 2006 6:34 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/762577

Please ~~rush~~. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Davis, Minh-Tam
Sent: Thursday, April 20, 2006 10:40 AM
To: Chan, Christina
Subject: Rush search request for 09/762577

Please search in commercial database, issued patent files, pGPUB and interference:

- 1) Oligomer search for SEQ ID NO:11
- 2) Oligomer search for the nucleic acid encoding SEQ ID NO:12.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 22, 2006, 09:11:41 ; Search time 6216 Seconds

(without alignments)
11394.295 Million cell updates/sec

Title: US-09-762-577B-11

Perfect score: 1246
Sequence: 1 CGGCGAGGAGCGCGCGG.....AGTGGGTTTCCCTGAGAGT 1246

Scoring table: Gapped 60.0, Gapex 60.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_rts.*
11: gb_sy.*
12: gb_un.*
13: gb_vt.*
14: gb_hcg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1228	98.6	1260	6	C0896991 Sequence
2	1228	98.6	1260	6	CS113085 Sequence
3	1228	98.6	1260	8	AF111388 Homo sapi
4	1228	98.6	1301	8	AY358835 Homo sapi
5	1228	98.6	1376	6	AX067715 Sequence
6	843	67.7	843	6	AX067716 Sequence
7	793	63.6	1312	6	C0896990 Sequence
8	793	63.6	1312	8	BC014475 Homo sapi
9	793	63.6	1370	8	AY358836 Homo sapi
10	783	62.8	840	6	BD167853 Survivin-
11	783	62.8	840	6	BD185365 Survivin-
12	742	59.6	1337	6	BD248275 DNA encod
13	742	59.6	1337	6	AR242238 Sequence
14	631	50.6	1021	8	AY517497 Homo sapi
15	601	48.2	1168	8	AF301009 Homo sapi
16	593	47.6	672	6	BD167852 Survivin-
17	593	47.6	672	6	BD185364 Survivin-
18	593	47.6	723	6	BD167851 Survivin-

19	593	47.6	723	6	BD185363 Survivin-
20	491	39.4	4810	8	HA309298 Homo sapi
21	491	39.4	184223	8	HA309298 Homo sapi
22	352	28.3	615	6	C0721033 Sequence
23	204	16.4	204	6	BD167849 Survivin-
24	204	16.4	204	6	BD185361 Survivin-
25	168	13.5	226	6	AR379789 Sequence
26	141	11.3	141	6	BD167850 Survivin-
27	141	11.3	141	6	BD185362 Survivin-
28	122	9.8	404	6	AX071974 Sequence
29	101	8.1	726	10	BV639843 Sequence
30	94	7.5	200	6	AR269653 Sequence
31	94	7.5	200	6	AR379842 Sequence
32	60	4.8	60	6	CQ543497 Sequence
33	34	2.7	34	11	CS000214 Sequence
34	26	2.1	26	6	BD167855 Survivin-
35	26	2.1	26	6	BD167860 Survivin-
36	26	2.1	26	6	BD185367 Survivin-
37	26	2.1	26	6	BD185372 Survivin-
38	26	2.1	264967	14	AC098373 Rattus no
39	25	2.0	25	6	BD248277 DNA encod
40	25	2.0	25	6	BD248278 DNA encod
41	25	2.0	25	6	AR242240 Sequence
42	25	2.0	25	6	AR242241 Sequence
43	25	2.0	225164	14	AC133320 Rattus no
44	25	2.0	235381	14	AC103031 Rattus no
45	24	1.9	24	6	BD167857 Survivin-

ALIGNMENTS

RESULT 1	C0896991	1260 bp	DNA	linear	PAT 08-NOV-2004
LOCUS	C0896991	Sequence 11 from Patent WO2004091388.			
DEFINITION	C0896991				
ACCESSION	C0896991.1	GI:55581833			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominiidae; Homo.				
REFERENCE					
AUTHORS	Butz, K., Grnkovic-Martens, I. and Hoppe-Seyler, F.				
TITLE	LYVIN-SPECIFIC siRNAs FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS				
JOURNAL	Patent: WO 2004091388-A 11 28-OCT-2004;				
	Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts				
	(DE)				
FEATURES					
source	1..1260	Location/Qualifiers			
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
Query Match	98.6%; Score 1228; DB 6; Length 1260;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 1228;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Q1	19 GCGAGGCGCTGCTGCTATCTGCTGCTGCCAGAGGTGGGCGGGGCTCAGAGCTCGAG 78				
Q2	33 GCGAGGCGCTGCTGCTATCTGCTGCTGCCAGAGGTGGGCGGGGCTCAGAGCTCGAG 92				
Q3	79 AAGGCGAGCTGGGCGATATCTGAGATTGGCGCATCAGCCCAATTGCTGCGCAAACTG 138				
Q4	93 AAGGCGAGCTGGGCGATATCTGAGATTGGCGCATCAGCCCAATTGCTGCGCAAACTG 152				
Q5	139 GTCAGAGCAGGTGTTCCCTCCATGAGGAGCTTAAAGACAGTGCAGAGCTCGACCGTGA 198				
Q6	153 GTCAGAGCAGGTGTTCCCTCCATGAGGAGCTTAAAGACAGTGCAGAGCTCGACCGTGA 212				

[illegible]

Db 914 TGCAGGCTGCTGAGACCGCCCGCTGCTGATGCTTTGTCCTGGGCGCAGCTGGTC 973
Oy 919 TGTGCTGAGTGTGCCCCCGGCGCTGAGCTGTGCCCCATCTGCAGAGCCCGCTCCGACG 978
Db 974 TGTGCTGAGTGTGCCCCCGGCGCTGAGCTGTGCCCCATCTGCAGAGCCCGCTCCGACG 1033
Oy 979 CGCGTGGCGACCTTCTGCTGCTTCAAGCCAGGTGCCATGGCCGGCCAGGTGGGCTGCAGAGT 1038
Db 1034 CGCGTGGCGACCTTCTGCTGCTTCAAGCCAGGTGCCATGGCCGGCCAGGTGGGCTGCAGAGT 1093
Oy 1039 GGGCTCCCGTCCCTCTGCTGCTGCTTCAAGCTGTGAGTGTGAGGCTGAGGATGGAG 1098
Db 1094 GGGCTCCCGTCCCTCTGCTGCTGCTTCAAGCTGTGAGTGTGAGGCTGAGGATGGAG 1153
Oy 1099 AGCTGTGTTCATCCAGCAGCTGACAGCCCTGATTTCCCGACACCGCCAGGCTGAGAGA 1158
Db 1154 AGCTGTGTTCATCCAGCAGCTGACAGCCCTGATTTCCCGACACCGCCAGGCTGAGAGA 1213
Oy 1159 AGGAGCCCTTGGCTTGGGCTGGGGGATGGCTTAAGCTGATGCTTTGATGCTTCTGAT 1218
Db 1214 AGGAGCCCTTGGCTTGGGCTGGGGGATGGCTTAAGCTGATGCTTTGATGCTTCTGAT 1273
Oy 1219 AGAATTAAGTGGGTTTCCCTGAGAGT 1246
Db 1274 AGAATTAAGTGGGTTTCCCTGAGAGT 1301

RESULT 5
AX067715
LOCUS AX067715 1376 bp DNA linear PAT 19-JAN-2001
DEFINITION Sequence 1 from Patent WO0077201.
ACCESSION AX067715.1 GI:12329602
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Gomes, B.C., Kasof, G.M. and Prosser, J.C.
TITLE Lysin: inhibitor-of-apoptosis protein-3 (iap-3)
JOURNAL Patent: WO 0077201-A 1 21-DEC-2000;
Asciadeneca AB (SE)
FEATURES
source location/Qualifiers
1..1376
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.6%; Score 1228; DB 6; Length 1376;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 GGCAGGCTGTGCTATCCCTGCTGTGCTCCCAAGGTGGGCCCCGGGGCTCAGAGCTCCAG 78
Db 70 GGCAGGCTGTGCTATCCCTGCTGTGCTCCCAAGGTGGGCCCCGGGGCTCAGAGCTCCAG 129
Oy 79 AAGGGCCAGTGGGCGATTTGAGATTGGGCATAGCCCCCATTTGCTGCAAACTG 138
Db 130 AAGGGCCAGTGGGCGATTTGAGATTGGGCATAGCCCCCATTTGCTGCAAACTG 189
Oy 139 GTCAAGCCAGTGTTCCTTCATGAGACCTAAAGACAGTGCCTGCTGCAAGCTGCA 198
Db 190 GTCAAGCCAGTGTTCCTTCATGAGACCTAAAGACAGTGCCTGCTGCAAGCTGCA 249
Oy 199 CCACAGCCGAGCCTGCTGGGCGAGCGGTATGTGCCACGACGAGAGCGCTGTGAGACCCCGC 258
Db 250 CCACAGCCGAGCCTGCTGGGCGAGCGGTATGTGCCACGAGAGCGCTGTGAGACCCCGC 309
Oy 259 TCTTGGGCGAGCCCTGTCTAGAGCTGAGACCTGCAAGCGCTGGGACCAAGTGGATGG 318

Db 310 TCTTGGGCGAGCCCTGTGCTTCAAGGCTGAGACCTGCAAGAGCTTGGACCAAGTGGATGG 369
Oy 319 CAGATCCCTGGGCGAGCTGCGGCCCCCTGACAGAGAGAGAGAGAGAGGCGCGGGCC 378
Db 370 CAGATCCCTGGGCGAGCTGCGGCCCCCTGACAGAGAGAGAGAGAGAGGCGCGGGCC 429
Oy 379 ACCTTGTCCAGGGGGCTGCTTCCCGGCAAGGGCTTCTGAGAGTTGCGTCTGGCTCC 438
Db 430 ACCTTGTCCAGGGGGCTGCTTCCCGGCAAGGGCTTCTGAGAGTTGCGTCTGGCTCC 489
Oy 439 TTCTATAGCTGGCGGCTGACCTGCTGAGTGTGCAACCCAGAGCTGCTGCTGCGGCTTC 498
Db 490 TTCTATAGCTGGCGGCTGACCTGCTGAGTGTGCAACCCAGAGCTGCTGCTGCGGCTTC 549
Oy 499 TTCCACAGGCGCATCAGACAGAGTGAAGTGTCTTCTGCTATGAGGGGCTGACAGC 558
Db 550 TTCCACAGGCGCATCAGACAGAGTGAAGTGTCTTCTGCTATGAGGGGCTGACAGC 609
Oy 559 TGAAGCGCGGGGAGCAGACCCCTGAGCGAGATGCCAAGTGTGCCAGCTGTCAATTG 618
Db 610 TGAAGCGCGGGGAGCAGACCCCTGAGCGAGATGCCAAGTGTGCCAGCTGTCAATTG 669
Oy 619 CTGCTCCGCTCAAAAGGAAGAGACTTGTCCACAGTGTGACAGAGACTCACTCCACCTG 678
Db 670 CTGCTCCGCTCAAAAGGAAGAGACTTGTCCACAGTGTGACAGAGACTCACTCCACCTG 729
Oy 679 CTGGGCTCTTGGAGCCCGTGGAGAAACCGAAGACGAGCCCTGTGAGCCCTCCGTC 738
Db 730 CTGGGCTCTTGGAGCCCGTGGAGAAACCGAAGACGAGCCCTGTGAGCCCTCCGTC 789
Oy 739 CTGCTCTTGGAGTCCCTGAGCTGCGCAGACCCAGAGAGAGTCCAGTCTGAAGTGGC 798
Db 790 CTGCTCTTGGAGTCCCTGAGCTGCGCAGACCCAGAGAGAGTCCAGTCTGAAGTGGC 849
Oy 799 CAGAGCCAGAGAGCAGAGATGTGAGAGCCAGTGGGGGCTGCGAGAGAGAGAGAGC 858
Db 850 CAGAGCCAGAGAGCAGAGATGTGAGAGCCAGTGGGGGCTGCGAGAGAGAGAGAGC 909
Oy 859 TGCAGAGTGTGCTGAGACCGCGCGCTGCTCCATGCTCTTGTGCGGCTCGGCACTGGTC 918
Db 910 TGCAGAGTGTGCTGAGACCGCGCGCTGCTCCATGCTCTTGTGCGGCTCGGCACTGGTC 969
Oy 919 TGTGCTGAGTGTGCCCCCGGCTGAGCTGTGCCCCATCTGACAGAGCCCGCTCCGACG 978
Db 970 TGTGCTGAGTGTGCCCCCGGCTGAGCTGTGCCCCATCTGACAGAGCCCGCTCCGACG 1029
Oy 979 CGGCTGGGACCTTCCCTGCTGCTAGGCGCAGGTGCCATGGCCGGCCAGGTGGGCTGCAAGT 1038
Db 1030 CGGCTGGGACCTTCCCTGCTGCTAGGCGCAGGTGCCATGGCCGGCCAGGTGGGCTGCAAGT 1089
Oy 1039 GGGCTCCCGTCCCTCTGCTGCTGCTTGTGAGACTGTGTTCTGGGCTGCTGAGATGAGC 1098
Db 1090 GGGCTCCCGTCCCTCTGCTGCTGCTTGTGAGACTGTGTTCTGGGCTGCTGAGATGAGC 1149
Oy 1099 AGCTGTGTTCATCCAGCAGCTGACAGCCCTGATTTCCCGACACCGCCAGGCTGAGAGA 1158
Db 1150 AGCTGTGTTCATCCAGCAGCTGACAGCCCTGATTTCCCGACACCGCCAGGCTGAGAGA 1209
Oy 1159 AGGAGCCCTTGGCTTGGGCGTGGGGGATGGCTTAAGTGTACTGTTTGGATGCTTCTGAT 1218
Db 1210 AGGAGCCCTTGGCTTGGGCGTGGGGGATGGCTTAAGTGTACTGTTTGGATGCTTCTGAT 1269
Oy 1219 AGAATTAAGTGGGTTTCCCTGAGAGT 1246
Db 1270 AGAATTAAGTGGGTTTCCCTGAGAGT 1297

RESULT 6
AX067716
LOCUS AX067716 843 bp DNA linear PAT 19-JAN-2001
DEFINITION Sequence 2 from Patent WO0077201.
ACCESSION AX067716

VERSION AX067716.1 GI:12329603
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Gomes, B.C., Kasof, G.M. and Prosser, J.C.
TITLE Livin; inhibitor-of-apoptosis protein-3 (Iap-3)
JOURNAL Patent: WO 0077201-A 2 21-DEC-2000;
Astrazeneca AB (SE)
FEATURES
source 1..843
Location/Qualifiers
1..843
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 67.7%; Score 843; DB 6; Length 843;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 160 ATGGACCTTAAGA CAGTGGCCAA GTGCTGACCGTGACCA CAGCCGACCACTGGAGA 219
Db 1 ATGGAGCTTAAGA CAGTGGCCAA GTGCTGACCGTGACCA CAGCCGACCACTGGAGA 60
QY 220 GCCGGTATGTTGCC CAGCAGAGACCGTGTGACCCCGCTCTCTGGGACAGCCCTGTCTTA 279
Db 61 GCCGTATGTTGCC CAGCAGAGACCGTGTGACCCCGCTCTCTGGGACAGCCCTGTCTTA 120
QY 280 GGCCTGACACCTG CAGAGCCTGGGACCA CAGTGGATGGGACATCTCTGGGACAGCTGGG 339
Db 121 GGCCTGACACCTG CAGAGCCTGGGACCA CAGTGGATGGGACATCTCTGGGACAGCTGGG 180
QY 340 CCCCTGACAGAGA GAGAGAGAGAGAGGCGCCGGGACCACTTGTTCAGAGGGGCGCTGCG 399
Db 181 CCCCTGACAGAGA GAGAGAGAGAGAGGCGCCGGGACCACTTGTTCAGAGGGGCGCTGCG 240
QY 400 TTCCCGGCAATGG GCTCTGAGAGTGGCGTGGCTGCGCTCTCTCTCTCTCTCTCTCTCTCT 459
Db 241 TTCCCGGCAATGG GCTCTGAGAGTGGCGTGGCTGCGCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 460 GCTGAGGTGACAC CCGAGCTGTGAGTGTGCTGCGGCTTCTTCCACACAGAGCCATCAGAG 519
Db 301 GCTGAGGTGACAC CCGAGCTGTGAGTGTGCTGCGGCTTCTTCCACACAGAGCCATCAGAG 360
QY 520 AAGGTAGAGTCTT CTCTGCTATGGGGCTTGCAGAGCTGGAAGCGCGGGAGCAACCC 579
Db 361 AAGGTAGAGTCTT CTCTGCTATGGGGCTTGCAGAGCTGGAAGCGCGGGAGCAACCC 420
QY 580 TGGACGAGCATGC CAAAGTGTTCCTCCAGCTGTCAAGTCTCTCTCTCTCTCTCTCTCTCT 639
Db 421 TGGACGAGCATGC CAAAGTGTTCCTCCAGCTGTCAAGTCTCTCTCTCTCTCTCTCTCTCT 480
QY 640 GACTTGTTCACAG TGTGACAGAGACTCACTCCAGCTGTGAGTGTGAGTGTGAGTGTGAG 699
Db 481 GACTTGTTCACAG TGTGACAGAGACTCACTCCAGCTGTGAGTGTGAGTGTGAGTGTGAG 540
QY 700 GAAGAACCAGAAAG CAGCAGCCCTGTGGGCCCCCTCCGCTCTCTCTCTCTCTCTCTCTCT 759
Db 541 GAAGAACCAGAAAG CAGCAGCCCTGTGGGCCCCCTCCGCTCTCTCTCTCTCTCTCTCTCT 600
QY 760 CTGCCACACCCAG AAGAGAGAGGTCCAAGTGAAGTGGCCAGAGCCAGAGCCAGAGAT 819
Db 601 CTGCCACACCCAG AAGAGAGAGGTCCAAGTGAAGTGGCCAGAGCCAGAGCCAGAGAT 660
QY 820 GTGAGAGCAGACT GCGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
Db 661 GTGAGAGCAGACT GCGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 880 GCGGTGTCATGCT TTTGTGCGCGGACCACTGTCTGTGCTGAGTGTGAGTGTGAGTGTGAG 939

Db 721 GCCGTGCATGCTT TGTGCGCGGACCACTGTCTGTGCTGAGTGTGAGTGTGAGTGTGAG 780
QY 940 CTGACGCTGTGCCC CATCTGCAGAGCCCCCGTCCGACCGCGTGCAGCACTTCTGTGC 999
Db 781 CTGACGCTGTGCCC CATCTGCAGAGCCCCCGTCCGACCGCGTGCAGCACTTCTGTGC 840
QY 1000 TAG 1002
Db 841 TAG 843
RESULT 7
LOCUS CQ896990 1312 bp DNA linear PAT 08-NOV-2004
DEFINITION Sequence 10 from Patent WO2004091388.
ACCESSION CQ896990
VERSION CQ896990.1 GI:55581832
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Butz, K., Cynkovic-Mertens, I. and Hoppe-Seyler, F.
TITLE LIVIN-SPECIFIC siRNAs FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS
JOURNAL Patent: WO 2004091388-A 10 28-OCT-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)
FEATURES
source 1..1312
Location/Qualifiers
1..1312
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 63.6%; Score 793; DB 6; Length 1312;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 GGCAGGCTGTGCTAT CCTGCTGTCCTCCAGAGGTGGGCCCCGGGGGTGAGAGCTCCAG 78
Db 8 GGCAGGCTGTGCTAT CCTGCTGTCCTCCAGAGGTGGGCCCCGGGGGTGAGAGCTCCAG 67
QY 79 AAGGGCAGCTGGG CATATTCTGAGATTGGCCATCAGCCCCCATTTCTGTGAAACCTG 138
Db 68 AAGGGCAGCTGGG CATATTCTGAGATTGGCCATCAGCCCCCATTTCTGTGAAACCTG 127
QY 139 GTCAGAGCCAGTGT CCGCTCATGGGACCTAAAGACAGTGGCCAAAGTGGCCCTGCACCGTGA 198
Db 128 GTCAGAGCCAGTGT CCGCTCATGGGACCTAAAGACAGTGGCCAAAGTGGCCCTGCACCGTGA 187
QY 199 CCAAGCCGAGGCA CTGGGAGCGGATGATGATCCACGACAGAGAGCGTGTGAGACCCGCG 258
Db 188 CCAAGCCGAGGCA CTGGGAGCGGATGATGATCCACGACAGAGAGCGTGTGAGACCCGCG 247
QY 259 TCTCTGGGAGCCCT GTCCTGAGGCTTGAGACCTGAGAGCTGGGACCAAGTGAATGGG 318
Db 248 TCTCTGGGAGCCCT GTCCTGAGGCTTGAGACCTGAGAGCTGGGACCAAGTGAATGGG 307
QY 319 CAGATCCTGGGCA GCTGGGCGCCCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
Db 308 CAGATCCTGGGCA GCTGGGCGCCCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
QY 379 ACCTTGTCCAGG GGGGCTGCTTCCCGGCAATGGGCTTGAAGAGTGTGCTGTGAGCTTCC 438
Db 368 ACCTTGTCCAGG GGGGCTGCTTCCCGGCAATGGGCTTGAAGAGTGTGCTGTGAGCTTCC 427
QY 439 TTCTATGACTGG CCGCTGACTGCTGAGTGGCCAGCCGAGCTGCTGCTGCTGCTGCTGCTG 498
Db 428 TTCTATGACTGG CCGCTGACTGCTGAGTGGCCAGCCGAGCTGCTGCTGCTGCTGCTGCTG 487
QY 499 TTCACACAGGCC CATCAGAGCAAGGTGAGTGTCTTCTGCTATGGGGGCTGTGACAGAGC 558

```

Db      488 TTCCACACAGCGCCATCAGAGACAGGTGAGTCTTCTTCTGCTATAGGGGGCTGCAGAGC 547
Oy      559 TGAAGCGCGGGGAGCGACCCCTGAGCGAGCATGCCAAGTGTTCCAGCTGTGCACTTC 618
Db      548 TGAAGCGCGGGGAGCGACCCCTGAGCGAGCATGCCAAGTGTTCCAGCTGTGCACTTC 607
Oy      619 CTGCTCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTGCAGAGACATCTCCCACTG 678
Db      608 CTGCTCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTGCAGAGACATCTCCCACTG 667
Oy      679 CTGGGCTCCTGGGACCCCTGGGAAGACCGGAAGACGAGCCCTGTGGCCCTCCGCTC 738
Db      668 CTGGGCTCCTGGGACCCCTGGGAAGACCGGAAGACGAGCCCTGTGGCCCTCCGCTC 727
Oy      739 CTTGCTCTGTGGTACCTGTAGCTGCCACACCCAGAGAGAGAGTGTCAAGTGTGAGTCC 798
Db      728 CTTGCTCTGTGGTACCTGTAGCTGCCACACCCAGAGAGAGAGTGTCAAGTGTGAGTCC 787
Oy      799 CAGAGCCAGGAG 811
Db      788 CAGAGCCAGGAG 800

RESULT 8
LOCUS   BC014475      1312 bp      mRNA      linear      PRI 30-JUN-2004
DEFINITION Homo sapiens baculoviral IAP repeat-containing 7 (livin),
transcript variant 1, mRNA (cDNA clone MGC:23131 IMAGE:4859588),
complete cds.
ACCESSION BC014475
VERSION   BC014475.1 GI:15680240
KEYWORDS   MGC.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 1312)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stjepanovic,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheer,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Caciopri,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huliyil,S.W.,
            Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Scherchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzyzanski,M.I., Skalska,U., Smalins,D.E.,
            Schnerker,A., Schein,J.E., Jones,S.J., and Marra,M.A.
            Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
            12477932

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Rubin Laboratory

```

```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@ccgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Motin,
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lisa Prabh,
Parvaneh Saeedi, Jr Santos, Angeliq Schnerker, Ursula Skalska,
Duane Smalies, Jeff Scott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 34 Row: F Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21536419.

FEATURES
Source
Location/Qualifiers
1..1312
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:23131 IMAGE:4859588"
/tissue_type="Skin, melanotic melanoma, high MDR."
/clone_id="NIH_MGC_49"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
1..1312
/gene="BIRC7"
/note="synonyms: MI-IAP, KIAP, LIVIN, RNF50, MLIAF"
/db_xref="GeneID:79444"
/db_xref="MIM:605737"
149..1045
/gene="BIRC7"
/codon_start=1
/product="livin inhibitor of apoptosis, isoform alpha"
/protein_id="AAH14475.1"
/db_xref="GI:15680241"
/db_xref="GeneID:79444"
/db_xref="MIM:605737"
/translation="MGPKDSAKLHRPDSHMAAGDPQROCRPSLSPVLGDT
CRANDYDQGLIQLRLPTEBEEBEGATLSKGRPRGSGSELRASRYDPLTAE
VPELLAAEFHGHODKRCFTGGGLDSMKRDPWTEHAKMFPSCPLSKKR
DPVHSVETHSQLSWDPEBEDAPVAPVSPASYPPLPPTPRRVSQESASQEPG
VSPADQARAWVLEPPGARDVEAQLRLQERICKVCLDRAVSIIVFCGHLVCAECA
PGLQICRICAPVRSRVRTFLS"

ORIGIN
Query Match 63.6%; Score 793; DB 8; Length 1312;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      19 GGCAGGCTGTGCTTATCCCTGCTGCTCCAGAGGTGGGCGGGGGGTGAGAGCTCCAG 78
Db      8 GGCAGGCTGTGCTTATCCCTGCTGCTCCAGAGGTGGGCGGGGGGTGAGAGCTCCAG 67
Oy      79 AAGGCGCAGCTGGGATATTTCTGAGATTGGACATACAGCCCAATTTCTGTGCAAACTG 138
Db      68 AAGGCGCAGCTGGGATATTTCTGAGATTGGACATACAGCCCAATTTCTGTGCAAACTG 127
Oy      139 GTGAGAGCCAGTGTCTCTCCATAGGAGCTTAAAGACAGTGCAGAGCTGTGACCTGGA 198
Db      128 GTGAGAGCCAGTGTCTCTCCATAGGAGCTTAAAGACAGTGCAGAGCTGTGACCTGGA 187
Oy      199 CCACAGCCGAGCCACTGGGAGCGCGTATGTCCTCCAGAGAGAGCGCTGTGACCCCGC 258
Db      188 CCACAGCCGAGCCACTGGGAGCGCGTATGTCCTCCAGAGAGAGCGCTGTGACCCCGC 247
Oy      259 TCTCTGGGAGCCCTGTCTTAAAGCTTGAGACCTGAGAGAGCTGTGAGACCACTGTGATGG 318
Db      248 TCTCTGGGAGCCCTGTCTTAAAGCTTGAGACCTGAGAGAGCTGTGAGACCACTGTGATGG 307

```


QY	319	CAGATCCTGGGCGCAGCTGCGGGCCCTTCA	CA	GAGAGGAGAGAGAGAGAGGCGCGCGGCC	378
Db	308	CAGATCTCGGAGCCAGCTGCGGCGCCCTTGA <th>CA</th> <th>GAGAGGAGAGAGAGAGAGGCGCGCGGCC</th> <td>367</td>	CA	GAGAGGAGAGAGAGAGAGGCGCGCGGCC	367
QY	379	ACCTTGTCCAGGGGGCCTGCTTCCCGCGAT	GGGCTCT	AGAGAGTTGGCGTCTGGGCTCC	438
Db	368	ACCTTGTCCAGGGGGCCTGCTTCCCGGAT	GGGCTCT	AGAGAGTTGGCGTCTGGGCTCC	427
QY	439	TTCTATATACCTGGCGCGCTGACTGCTGAG <th>GTGCC</th> <th>ACCCGAGCTGCTGCTGCGGCTTC</th> <td>498</td>	GTGCC	ACCCGAGCTGCTGCTGCGGCTTC	498
Db	428	TTCTATATACCTGGCGCGCTGACTGCTGAG <th>GTGCC</th> <th>ACCCGAGCTGCTGCTGCGGCTTC</th> <td>487</td>	GTGCC	ACCCGAGCTGCTGCTGCGGCTTC	487
QY	499	TTTCACACAGAGCCATCAGACACAGATGAT <th>GTGCTTT</th> <th>CTTCTGCTATATAGGGGCGCTGCAAGC</th> <td>558</td>	GTGCTTT	CTTCTGCTATATAGGGGCGCTGCAAGC	558
Db	488	TTTCACACAGAGCCATCAGACACAGATGAT <th>GTGCTTT</th> <th>CTTCTGCTATATAGGGGCGCTGCAAGC</th> <td>547</td>	GTGCTTT	CTTCTGCTATATAGGGGCGCTGCAAGC	547
QY	559	TGGAAGCGCGGGGACGACCCCTTGAGCG <th>AGCATGCC</th> <th>AAAGTGTTCCCGACGTGTCAGTTC</th> <td>618</td>	AGCATGCC	AAAGTGTTCCCGACGTGTCAGTTC	618
Db	548	TGGAAGCGCGGGGACGACCCCTTGAGCG <th>AGCATGCC</th> <th>AAAGTGTTCCCGACGTGTCAGTTC</th> <td>607</td>	AGCATGCC	AAAGTGTTCCCGACGTGTCAGTTC	607
QY	619	CTGCTCCGGTCAAAAAGAAAGAGACTTGT <th>GTCCACAGTGTCC</th> <th>ACAGAGACTCACTTCCACGCTG</th> <td>678</td>	GTCCACAGTGTCC	ACAGAGACTCACTTCCACGCTG	678
Db	608	CTGCTCCGGTCAAAAAGAAAGAGACTTGT <th>GTCCACAGTGTCC</th> <th>ACAGAGACTCACTTCCACGCTG</th> <td>667</td>	GTCCACAGTGTCC	ACAGAGACTCACTTCCACGCTG	667
QY	679	CTGGGCTCCTTGAGACCCGTGGGAAAGA <th>CCGGAAGACG</th> <th>ACCCCTGTGTGCGCCCTTCCGCTC</th> <td>738</td>	CCGGAAGACG	ACCCCTGTGTGCGCCCTTCCGCTC	738
Db	668	CTGGGCTCCTTGAGACCCGTGGGAAAGA <th>CCGGAAGACG</th> <th>ACCCCTGTGTGCGCCCTTCCGCTC</th> <td>727</td>	CCGGAAGACG	ACCCCTGTGTGCGCCCTTCCGCTC	727
QY	739	CCGTGCTCTGGGGTACCCCTAGCTGCCCC <th>ACACCCAGAGAGAG</th> <th>GTCCAGTCTTGAAGATGCC</th> <td>798</td>	ACACCCAGAGAGAG	GTCCAGTCTTGAAGATGCC	798
Db	728	CCGTGCTCTGGGGTACCCCTAGCTGCCCC <th>ACACCCAGAGAGAG</th> <th>GTCCAGTCTTGAAGATGCC</th> <td>787</td>	ACACCCAGAGAGAG	GTCCAGTCTTGAAGATGCC	787
QY	799	CAGAGCCAGGAG <td>811</td> <td></td> <td></td>	811		
Db	788	CAGAGCCAGGAG <td>800</td> <td></td> <td></td>	800		
RESULT 9					
AY358836					
LOCUS	AY358836	1370 bp	mRNA	linear	PRI 03-OCT-2003
DEFINITION	Home sapiens clone DNA172970 LIVIN	(UNQ5800)	mRNA,	complete cds.	
ACCESSION	AY358836				
VERSION	AY358836.1	GI:37182789			
KEYWORDS	FLI CDNA.				
SOURCE	Home sapiens (human)				
ORGANISM	Home sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 1370)				
AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Batton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Weiland,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.				
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment				
JOURNAL	Genome Res.	13 (10),	2265-2270	(2003)	
PUBMED	12975309				
REFERENCE	2 (bases 1 to 1370)				
AUTHORS	Clark,H.F.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-AGC-2003)				
FEATURES	1 DNA Way, South San Francisco, CA 94080, USA				
source	1. 1370				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				

```

gene
CDS
/db_xref="taxon:9606"
/clone="DNA172970"
1..1370
/locus_tag="UNQ5800"
215..1111
/locus_tag="UNQ5800"
/note="PRO21344"
/codon_start=1
/product="IIVIN"
/protein_id="AA09195.1"
/db_xref="GI:37182790"
/translation="MGPKDSAKCLHRPQESHMAAGDPTQERCGPSLGSFVPLGDT
CRANDYDGOILQGLRLPTEEBEEGAGATLSRGPAPMGSEELRLASFDFWLTLE
VPELLAAGFPHHQDQKVCFCFECYGLQSWKRGDDPMTENHAKMFCSCILLSKGR
DVSIVQETHSOLLGSDPWEERPDAAVPVAPSVASGYPELPTREEVQSSAEPQGG
VSPAEARANWVLEPFGARDVEQRLRLQEBRTICKCLDRAVSIIVFCGHLVCAECA
PGDLQCTICAPVNSRVRLFLS"

```

Query Match 63.6%; Score 793; DB 8; Length 1370;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	19	GGCAGAGCCCTGGGACCTATCCCTGCTGTCCCAAGGATGGGCCCGGGGGTTCAGAGCTCCAG	78
Db	74	GGCAGAGCCCTGGGACCTATCCCTGCTGTCCCAAGGATGGGCCCGGGGGTTCAGAGCTCCAG	13
QY	79	AAGGCGCAGCTGGGCATATTCTGAGATTGGCATTCAGACCCCATTTCTGTCTCAAACTCG	13
Db	134	AAGGCGCAGCTGGGCATATTCTGAGATTGGCATTCAGACCCCATTTCTGTCTCAAACTCG	19
QY	139	GTCAAGCCAGTGTTCCTCTCATGGGACCTTAAAGACAGTGCAGTGCCTGACCCGTGA	191
Db	194	GTCAAGCCAGTGTTCCTCTCATGGGACCTTAAAGACAGTGCAGTGCCTGACCCGTGA	25
QY	199	CCACAGCCGAGCCACTGGGAGCCGGGATTTGGTCCACGACAGACCGCTGTGAAACCCGC	25
Db	254	CCACAGCCGAGCCACTGGGAGCCGGGATTTGGTCCACGACAGACCGCTGTGAAACCCGC	31
QY	259	TCTGTGGGCAAGCCCTGTCTTAAGGCTTGACAACCTTGAGACCTTGAGACCAAGTGGATGG	31
Db	314	TCTGTGGGCAAGCCCTGTCTTAAGGCTTGACAACCTTGAGACCTTGAGACCAAGTGGATGG	37
QY	319	CAGATCCTGGGCCAAGCTGCGGGCCCTCTGACAGAGAGAAAGAGAGAGAGGCGCGGGGCC	37
Db	374	CAGATCCTGGGCCAAGCTGCGGGCCCTCTGACAGAGAGAAAGAGAGAGAGGCGGGGCC	43
QY	379	ACCTGTGTCAGAGGGGCGCTGCTTCCCGGCATAGGGGCTGAGAGATTGAGTGGCCCTCC	43
Db	434	ACCTGTGTCAGAGGGGCGCTGCTTCCCGGCATAGGGGCTGAGAGATTGAGTGGCCCTCC	49
QY	439	TTCTATATACCTGGCCGCTGACTGTGAGGTGCCACCCGAGCTGGCTGTGCCGGCTTC	49
Db	494	TTCTATATACCTGGCCGCTGACTGTGAGGTGCCACCCGAGCTGGCTGTGCCGGCTTC	55
QY	499	TTCCACACAGGCCCATAGAGCAAGGGTAGAGTCTTCTGTCTATGGGGGCTTGCAGAGC	55
Db	554	TTCCACACAGGCCCATAGAGCAAGGGTAGAGTCTTCTGTCTATGGGGGCTTGCAGAGC	61
QY	559	TGAAAGCGCGGGAGCAGACCCCTTGACAGAGCATGCTCAAGTGGTTCGCCAGCTGCAGTTC	61
Db	614	TGAAAGCGCGGGAGCAGACCCCTTGACAGAGCATGCTCAAGTGGTTCGCCAGCTGCAGTTC	67
QY	619	CTGCTCCGGTCAAAAGAGAGACTTTGTTCACAGTGTGCAGAGAGACTCACTCCAGCTG	67
Db	674	CTGCTCCGGTCAAAAGAGAGACTTTGTTCACAGTGTGCAGAGAGACTCACTCCAGCTG	73
QY	679	CTGGGCTCTGGGACCCGTGGAGAAACCGGAAACGAGCCCGTGTGGCCCTCCCTCGTC	73
Db	734	CTGGGCTCTGGGACCCGTGGAGAAACCGGAAACGAGCCCGTGTGGCCCTCCCTCGTC	79
QY	739	CTGTGCTTGGGATACCTTGAGCTGGCCACACGAGAGAGGTTCAGTCTGAAAGTGC	79

Db 794 CCGCCTCTGGGTACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTGC 853

Qy 799 CAGAGCCAGAG 811

Db 854 CAGAGCCAGAG 866

RESULT 10

BD167853 840 bp DNA linear PAT 17-JUN-2003

LOCUS Survivin-like polypeptide and its DNA.

DEFINITION BD167853

ACCESSION BD167853.1 GI:27873665

VERSION WO 0233071-A/5.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 840)

AUTHORS Tanaka,H. and Kaieda,I.

TITLE Survivin-like polypeptide and its DNA

JOURNAL Patent: WO 0233071-A 5 25-APR-2002; TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TANAKA,ISAO KAIEDA

COMMENT OS Homo sapiens (human)

PN WO 0233071-A/5

PD 25-APR-2002

PF 16-OCT-2001 WO 2001JP009071

PR 17-OCT-2000 JP 00P 316721.20-DEC-2000 JP 00P 366809 PI

HIROSHI TANAKA,ISAO KAIEDA

PC C12N15/09,C12N15/12,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/10, C12P21/02,C07K16/18,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50, PC A61K31/711, A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00 CC Survivin-like polypeptide and its DNA

PH Key Location/Qualifiers

FT source 1. 840 /organism='Homo sapiens (human)'. /location/Qualifiers 1. 840 /organism='Homo sapiens (human)'. /mol_type='genomic DNA' /db_xref='taxon:9606'

FEATURES

source

ORIGIN

Query Match 62.8%; Score 783; DB 6; Length 840;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 833; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 166 CCTAAGACAGTGCCTGCTGACCGTGGACCAAGCCGAGCCAGCTGGGACAGCCGCT 225

Db 7 CCTAAGACAGTGCCTGCTGACCGTGGACCAAGCCGAGCCAGCTGGGACAGCCGCT 66

Qy 226 GATGTCCTCCAGCAGAGCGCTGTGAGACCCGCTTCTGGGAGAGCCCTGTCTTGAAGCTG 285

Db 67 GATGTCCTCCAGCAGAGCGCTGTGAGACCCGCTTCTGGGAGAGCCCTGTCTTGAAGCTG 126

Qy 286 GACACCTGACAGCTGGGACCAAGCTGGATGGGAGATCTGGGACAGCTGGGACAGCTGG 345

Db 127 GACACCTGACAGCTGGGACCAAGCTGGATGGGAGATCTGGGACAGCTGGGACAGCTGG 186

Qy 346 ACAG 405

Db 187 ACAG 246

Qy 406 GGCATGGGCTCTGAGAGAGTGGCTGTGAGCTTCTTCTTGAAGCTGGGACAGCTGGAG 465

Db 247 GGCATGGGCTCTGAGAGAGTGGCTGTGAGCTTCTTCTTGAAGCTGGGACAGCTGGAG 306

Qy 466 GTGCACCCGAGAGCTGGCTGTGAGCTGGCTTCTTCAAGAGGAGCATCAGAGCAAGAGT 525

Db 307 GTGCCACCCAGAGCTGTGCTGCTGCTGCTGCTTCTTCCACACAGGCAATCAGAGCAAGT 366

Qy 526 AGGTGCTTCTTCTGCTATGGGGGCTGACAGAGCTGAGAGCGCGGAGAGACCTCTGACG 585

Db 367 AGGTGCTTCTTCTGCTATGGGGGCTGACAGAGCTGAGAGCGCGGAGAGACCTCTGACG 426

Qy 586 GAGCATGCAAGTGTTCCTCCAGCTGTCAAGTCTCTGCTCCGGTCAAAAAGAGAGACTTT 645

Db 427 GAGCATGCAAGTGTTCCTCCAGCTGTCAAGTCTCTGCTCCGGTCAAAAAGAGAGACTTT 486

Qy 646 GTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTCTGAGAGCCCGTGGAGAGAA 705

Db 487 GTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGCTCTGAGAGCCCGTGGAGAGAA 546

Qy 706 CCGGAG 765

Db 547 CCGGAG 606

Qy 766 ACACCCAG 825

Db 607 ACACCCAG 666

Qy 826 GCGAGCTGCGCGCGCTGACAG 885

Db 667 GCGAGCTGCGCGCGCTGACAG 726

Qy 886 TCCATGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 945

Db 727 TCCATGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786

Qy 946 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 999

Db 787 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

RESULT 11

BD185365 840 bp DNA linear PAT 17-JUN-2003

LOCUS Survivin-like polypeptide and its DNA.

DEFINITION BD185365

ACCESSION BD185365.1 GI:31877565

VERSION JP 2002355062-A 5 10-DEC-2002;

KEYWORDS TAKEDA CHEMICAL INDUSTRIES LTD

SOURCE OS Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 840)

AUTHORS Tanaka,H. and Kaieda,I.

TITLE Survivin-like polypeptide and its DNA

JOURNAL Patent: JP 2002355062-A 5 10-DEC-2002;

COMMENT OS Homo sapiens (human)

PN JP 2002355062-A/5

PD 10-DEC-2002

PF 16-OCT-2001 JP 2001318533

PI HIROSHI TANAKA,ISAO KAIEDA

PC C12N15/09,A61K31/7088,A61K38/55,A61K39/395,A61K39/395,A61K48/00,A61P35/00, A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19, PC C12N1/21 C12N15/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50, PC G01N33/53, G01N33/56,G01N33/574,C12N15/00,C12N5/00,A61K37/64 CC Survivin-like polypeptide and its DNA

PH Key Location/Qualifiers

FT source 1. 840 /organism='Homo sapiens (human)'. /location/Qualifiers 1. 840 /organism='Homo sapiens (human)'. /mol_type='genomic DNA' /db_xref='taxon:9606'

FEATURES

source

ORIGIN

Query Match 62.8%; Score 783; DB 6; Length 840;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 833; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 166 CCTAAGACAGTGGCCAAAGTGGCTGACACCGTGGACCAAGCCGAGCCATGGGACGCGGT 225
Db 7 CCTAAGACAGTGGCCAAAGTGGCTGACACCGTGGACCAAGCCGAGCCATGGGACGCGGT 66
QY 226 GATGTCCTCCACGACGAGAGCGCTGTGAACCCCGCTCTCTGAGGACCCCTGTCTTAGGCTTG 285
Db 67 GATGTCCTCCACGACGAGAGCGCTGTGAACCCCGCTCTCTGAGGACCCCTGTCTTAGGCTTG 126
QY 286 GACACCTGGAGAGCGCTGGAGCCAGTGGATGGAGATCTTGGGCCAGCTGCGGCCCTTG 345
Db 127 GACACCTGGAGAGCGCTGGAGCCAGTGGATGGAGATCTTGGGCCAGCTGCGGCCCTTG 186
QY 346 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
Db 187 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY 406 GGCATGGGCTCTTGAGAGAGTTCCTGCTGCTCTCTTATGACTGGCCGCTGACTGCTGAG 465
Db 247 GGCATGGGCTCTTGAGAGAGTTCCTGCTGCTCTCTTATGACTGGCCGCTGACTGCTGAG 306
QY 466 GTGCCACCCGAGCTGCTGAGCTGCTGAGCGCTGCTTCCACAGAGCCATGAGACAAAGTGG 525
Db 307 GTGCCACCCGAGCTGCTGAGCTGCTGAGCGCTGCTTCCACAGAGCCATGAGACAAAGTGG 366
QY 526 AGGTGCTTCTTCTGCTATGAGGAGGCTTGACAGCTGAGAGCGGAGAGACCCCTGAGAG 585
Db 367 AGGTGCTTCTTCTGCTATGAGGAGGCTTGACAGCTGAGAGCGGAGAGACCCCTGAGAG 426
QY 586 GAGCATGGCAAGGTGTTCCCGACCTGTCAGTTCCTCTCCGCTCAAAAGAGAGACTTT 645
Db 427 GAGCATGGCAAGGTGTTCCCGACCTGTCAGTTCCTCTCCGCTCAAAAGAGAGACTTT 486
QY 646 GTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGGGCTCCGAGGAGCCGAGGAGAGAA 705
Db 487 GTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGGGCTCCGAGGAGCCGAGGAGAGAA 546
QY 706 CGGAGAGAGCGAGCGCTGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
Db 547 CGGAGAGAGCGAGCGCTGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
QY 766 ACAACCCAGAGAGAGAGTCCAGTCTGAAAGTGCACAGAGCCAGAGCCAGAGAGATGGAG 825
Db 607 ACAACCCAGAGAGAGAGTCCAGTCTGAAAGTGCACAGAGCCAGAGCCAGAGAGATGGAG 666
QY 826 GCGCACTGCGGCGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
Db 667 GCGCACTGCGGCGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
QY 886 TCCATGCTTCTTGTGCGCGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 945
Db 727 TCCATGCTTCTTGTGCGCGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
QY 946 CTGTGCGCCATGTGACAGAGCCCGCTGCGAGCCGCTGCGAGCCCTTCTGCTGCTGCTGCT 999
Db 787 CTGTGCGCCATGTGACAGAGCCCGCTGCGAGCCGCTGCGAGCCCTTCTGCTGCTGCTGCT 840

```

RESULT 12

BD248275

LOCUS BD248275 1337 bp DNA linear PAT 17-JUL-2003
 DEFINITION DNA encoding human apoptosis inhibitor, protein HIPA3.
 ACCESSION BD248275.1 GI:33058045
 VERSION JP 2002524039-A/1.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS Deng G., Lin J.H. and Morser M.J.
 TITLE DNA encoding human apoptosis inhibitor, protein HIPA3
 JOURNAL Patent: JP 2002524039-A 1 06-AUG-2002;
 COMMENT
 OS Homo sapiens (human)
 PN JP 2002524039-A/1
 PD 06-AUG-2002
 PF 23-JUL-1999 JP 2000563771
 PR 31-JUL-1998 US 09/127928
 PI GANGL DENG, JIANG HUEY LIN, MICHAEL JOHN MORSER
 PC C12N15/09, A61K31/7088, A61K35/76, A61K38/00, A61K45/00,
 PC A61K48/00,
 PC A61P9/04, A61P9/10, A61P25/14, A61P25/28, A61P31/12, A61P35/00, PC
 A61P37/02,
 PC C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
 , C12P21/02, C12Q1/68,
 PC G01N33/15, G01N33/50, G01N33/53, G01N33/56, C12N15/00,
 PC C12N5/00,
 PC A61K37/02, A61K37/54
 CC DNA encoding human apoptosis inhibitor, protein HIPA3 FH Key

FEATURES
 source
 FT CDS Location/Qualifiers
 1..1337
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 59.6%; Score 742; DB 6; Length 1337;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 19 GGCAGGCGCTGCTATCCCTGCTGTCCTCCAGAGGTGGCCCGGGGTACAGAGCTCCAG 78
Db 29 GGCAGGCGCTGCTATCCCTGCTGTCCTCCAGAGGTGGCCCGGGGTACAGAGCTCCAG 88
QY 79 AAGGGCCAGCTGGGCAATATCTGAGATGGGCATCCAGCCCATTTCTGTGCAAACTGG 138
Db 89 AAGGGCCAGCTGGGCAATATCTGAGATGGGCATCCAGCCCATTTCTGTGCAAACTGG 148
QY 139 GTACAGCCAGTGTTCCTTCATGGAGCCTAAAGACAGTGCACAGTGCCTGACCCGTGA 198
Db 149 GTACAGCCAGTGTTCCTTCATGGAGCCTAAAGACAGTGCACAGTGCCTGACCCGTGA 208
QY 199 CCAAGCCGAGCCACTGGGAGCGGCTGATGGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258
Db 209 CCAAGCCGAGCCACTGGGAGCGGCTGATGGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 268
QY 259 TCTGTGGGACGCTGCTCTAGAGCTGACACCTGACAGCCCTGGAGCCACGTGATGG 318
Db 269 TCTGTGGGACGCTGCTCTAGAGCTGACACCTGACAGCCCTGGAGCCACGTGATGG 328
QY 319 CAGATCTGGGAGCAGTGGGCGCCCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
Db 329 CAGATCTGGGAGCAGTGGGCGCCCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 388
QY 379 ACCTTGTCCAGGGGGCTGCTTCCCGCATGGGCTCTGAGAGAGTGGCTGAGCTGCTG 438
Db 389 ACCTTGTCCAGGGGGCTGCTTCCCGCATGGGCTCTGAGAGAGTGGCTGAGCTGCTG 448
QY 439 TTCTATGACTGGCCGCTGACCTGCTGAGTGCACCCGAGAGCTGCTGCTGCTGCTGCTGCT 498
Db 449 TTCTATGACTGGCCGCTGACCTGCTGAGTGCACCCGAGAGCTGCTGCTGCTGCTGCTGCT 508
QY 499 TTCCACACAGGCCATCAGAGCAAGGTGAGGTCTTCTGCTATGAGGGGCTGAGAGG 558
Db 509 TTCCACACAGGCCATCAGAGCAAGGTGAGGTCTTCTGCTATGAGGGGCTGAGAGG 568
QY 559 TGGAGCGCGGGAGCAGACCCCTGACGAGAGCATGCAAGGTGGTTCCTCCAGCTGCTGAGTTCC 618

```

Db 569 TGAAGCGCGGGAGAGACCCCTGAGCGAGCATGCCAAGTGTTCCTCCAGCTGTCAATTC 628
Qy 619 CTGCTCCGGTCAAAAGAGAAAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 678
Db 629 CTGCTCCGGTCAAAAGAGAAAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 688
Qy 679 CTGGGCTTCTGGGACCCCTGGGAGAACCGGAAAGCAGCCCTGTGTGGCCCTCCGCTC 738
Db 689 CTGGGCTTCTGGGACCCCTGGGAGAACCGGAAAGCAGCCCTGTGTGGCCCTCCGCTC 748
Qy 739 CCTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTCC 798
Db 749 CCTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTCC 808
Qy 799 CAGAGCCAGGAG 811
Db 809 CAGAGCCAGGAG 821

RESULT 13
LOCUS AR242238 1337 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6472172.
ACCESSION AR242238
VERSION AR242238.1 GI:27288060
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1337)
AUTHORS Deng, G., Lin, J.-H. and Morser, M.J.
TITLE DNA encoding a novel human inhibitor-of-apoptosis protein
JOURNAL Patent: US 6472172-A 1 29-OCT-2002;
Schering Aktiengesellschaft; Berlin;
DEX;

FEATURES
source 1.1337
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 59.6%; Score 742; DB 6; Length 1337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 GGCAGGCTGTGCTTATCCCTGCTGTCGCCAGGTGGGCCCGGGGGTCAAGAGCTCCAG 78
Db 29 GGCAGGCTGTGCTTATCCCTGCTGTCGCCAGGTGGGCCCGGGGGTCAAGAGCTCCAG 88
Qy 79 AAGGCCAGCTGGGCAATTTTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAACCTG 138
Db 89 AAGGCCAGCTGGGCAATTTTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAACCTG 148
Qy 139 GTCAGAGCCAGTGTTCCTCCATGAGGACCTTAAGACAGTGCAGTGCCTGCAACCTG 198
Db 149 GTCAGAGCCAGTGTTCCTCCATGAGGACCTTAAGACAGTGCAGTGCCTGCAACCTG 208
Qy 199 CCAAGGCCAGGCACTGGGAGCGGAGTATGTCCTCCAGCAGAGCCCTGTGACCCGCG 258
Db 209 CCAAGGCCAGGCACTGGGAGCGGAGTATGTCCTCCAGCAGAGCCCTGTGACCCGCG 268
Qy 259 TCTTCTGGGAGCCCTGTGCTAGAGCTTGAGACCTGCAAGCTTGGGACCAAGTGAATGG 318
Db 269 TCTTCTGGGAGCCCTGTGCTAGAGCTTGAGACCTGCAAGCTTGGGACCAAGTGAATGG 328
Qy 319 CAGATCTGGGCGCAGCTGGCGGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
Db 329 CAGATCTGGGCGCAGCTGGCGGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 388
Qy 379 ACCTTGTTCAGAGGGGCGCTTCCCGGACATGGGACTCTGAGAGATTGCGTCTGGCTCC 438
Db 389 ACCTTGTTCAGAGGGGCGCTTCCCGGACATGGGACTCTGAGAGATTGCGTCTGGCTCC 448

Qy 439 TTCTATGACTGGCCCGCTGACTGCTGAGTGCACCCGAGCTGCTGCTGCTGCCGCTTC 498
Db 449 TTCTATGACTGGCCCGCTGACTGCTGAGTGCACCCGAGCTGCTGCTGCTGCCGCTTC 508
Qy 499 TTCCACACAGGCACTAGAGCAAGGTGAGTGTCTTCTTGTGATATGGGGGCTCCAGAGC 558
Db 509 TTCCACACAGGCACTAGAGCAAGGTGAGTGTCTTCTTGTGATATGGGGGCTCCAGAGC 568
Qy 559 TGAAGCGCGGGAGCAGCCCTGGAACGAGCATGCCAAGTGTTCCTCCAGCTGCAATTC 618
Db 569 TGAAGCGCGGGAGCAGCCCTGGAACGAGCATGCCAAGTGTTCCTCCAGCTGCAATTC 628
Qy 619 CTGCTCCGGTCAAAAGAGAAAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 678
Db 629 CTGCTCCGGTCAAAAGAGAAAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 688
Qy 679 CTGGGCTCTGGGACCCCTGGGAGAACCGGAAAGACGACCCCTGTGTGGCCCTCCGCTC 738
Db 689 CTGGGCTCTGGGACCCCTGGGAGAACCGGAAAGACGACCCCTGTGTGGCCCTCCGCTC 748
Qy 739 CTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTCC 798
Db 749 CTGCTCTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGTCC 808
Qy 799 CAGAGCCAGGAG 811
Db 809 CAGAGCCAGGAG 821

RESULT 14
LOCUS AY517497 1021 bp mRNA linear PRI 03-FEB-2004
DEFINITION Homo sapiens baculoviral IAP repeat-containing 7 (BIRC7) mRNA,
complete cds, alternatively spliced.
ACCESSION AY517497
VERSION AY517497.1 GI:41387694
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1021)
AUTHORS Li, H., Ke, R., Wang, C., Zhou, G., Shen, C., Lin, L. and Yang, S.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2004) Guangzhou Fulenggen Co., Ltd., 5/F.,
Guangzhou Entrepreneur Park for Overseas Chinese Scholars, 11
Baoshi Rd., GETDD, Guangzhou, Guangdong 510730, China

FEATURES
source 1.1021
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
/map="20q13.3"
1.1021
/gene="BIRC7"
/note="synonym: KIAF, LIVIN, MLIAF, RNF50, ML-IAP"
1.675
/gene="BIRC7"
/note="alternatively spliced"
/codon_start=1
/product="baculoviral IAP repeat-containing 7"
/protein_id="AA501729.1"
/db_xref="GI:41387695"
/translation="MGKPSAKCIHQHGPSPSHMAADGSPORBCGRSLGSPVLGDT
CRAMDVVDGQILUQLRPLTBEERBEGATLSRPAFPQMGSEBELSLASPIWPLTAE
VPELILAAAGFPHTGHODVRCEFCYGGIQQSWRGDDPWTEHAKWFPSCQPLRSRGR
DFHVSVOETHSOLIGSMDEPDEDAAPVAPSVPAAGYPDELPTPREVOSGSAQBPGA
GRGPG"

ORIGIN

Query Match 50.6%; Score 631; DB 8; Length 1021;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 ATGGGACCTTAAAGACAGTGGCCAAAGTGCCTGACCGTGGACACAGCCGAGCCACTGGGCA 219
 Db 1 ATGGGACCTTAAAGACAGTGGCCAAAGTGCCTGACCGTGGACACAGCCGAGCCACTGGGCA 60

QY 220 GCCGATATGATGCTCCACGACGAGACCGCTGTGAAACCCCGCTCTGTGGGCAAGCCCTGTCTTA 279
 Db 61 GCCGATATGATGCTCCACGACGAGCCGCTGTGAAACCCCGCTCTGTGGGCAAGCCCTGTCTTA 120

QY 280 GGCCTGACACCTGACAGAGCCTGGGACCAAGTGGATGGGAGATCTCTGGGACCAAGCTGGCG 339
 Db 121 GGCCTGACACCTGACAGAGCCTGGGACCAAGTGGATGGGAGATCTCTGGGACCAAGCTGGCG 180

QY 340 CCCCTGACAG 399
 Db 181 CCCCTGACAG 240

QY 400 TTCCCGGACATGGGCTCTGAGAGAGTGGCTGCTGCTGCTCTCTTATATGACTGGCCGCTGACT 459
 Db 241 TTCCCGGACATGGGCTCTGAGAGAGTGGCTGCTGCTGCTCTCTTATATGACTGGCCGCTGACT 300

QY 460 GCTGAGAGTGCACCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
 Db 301 GCTGAGAGTGCACCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

QY 520 AAGTGAAGTGTCTTCTTCTGCTATGAGAGGCTGACAGAGCTGGAAGCGCGGAGACGACCCC 579
 Db 361 AAGTGAAGTGTCTTCTTCTGCTATGAGAGGCTGACAGAGCTGGAAGCGCGGAGACGACCCC 420

QY 580 TGGACGAGAGATGCAAGTGGTTCCTCCAGTGTCACTCTGCTCCGGTCAAAAGAGAGA 639
 Db 421 TGGACGAGAGATGCAAGTGGTTCCTCCAGTGTCACTCTGCTCCGGTCAAAAGAGAGA 480

QY 640 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGAGGCTCTGAGACCCGCTGG 699
 Db 481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGAGGCTCTGAGACCCGCTGG 540

QY 700 GAAGAACCAGGAAGACGACCCCTGTGGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
 Db 541 GAAGAACCAGGAAGACGACCCCTGTGGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY 760 CTGCCACACCCAGAGAGAGAGTCCAGTCTG 790
 Db 601 CTGCCACACCCAGAGAGAGAGTCCAGTCTG 631

RESULT 15
 AF301009
 LOCUS AF301009 1168 bp mRNA linear PRI 05-DEC-2000
 DEFINITION Homo sapiens inhibitor of apoptosis protein K1AP mRNA, complete cds.
 ACCESSION AF301009
 VERSION AF301009.1 GI:11545502
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo; 1 (bases 1 to 1168)
 Lin, J.-H., Deng, G., Huang, Q. and Morser, J.,
 A Novel member of the inhibitor of apoptosis protein family
 Biochem. Biophys. Res. Commun. (2000) In press
 2 (bases 1 to 1168)
 Lin, J.-H., Deng, G. and Morser, J.,
 Direct Submission
 Submitted (29-AUG-2000) Cardiovascular Research, Berlex Biosciences
 Inc., 15049 San Pablo Ave., Richmond, CA 94804, USA
 FEATURES
 source 1..1168

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="20"
 /map="20q13.3"
 /feature_type="kidney"
 /dev_stage="fetus"
 1..897
 /codon_start=1
 /product="inhibitor of apoptosis protein K1AP"
 /protein_id="AAG37878.1"
 /db_xref="GI:11545503"
 /translation="MGPKDSAKCLHRRGPSPHMAAGDPTQERCPRLSPVGLPT
 CRAMDHYDGIQLRLPTEEBEAGATLSRGPARGMSEELRLASVDPMTAE
 VPPELLAAGFTFHGDVKRCFPCYAGLDSMRGDDPMTEHMKPSPCOPLRSKR
 DFVHSVQETHSLLGSWDPWEEPPDAPVAPSPVPSYRELPTRPREVQESLQEREG
 VSPAEARAWVLEPPGARVYEAQLRLQERITCKVLDRAVSIIVFPCGLVCABCA
 PGLQLCPCRAVPASRVRLPLS"
 259..462
 /note="Region: BIR domain"
 721..867
 /note="Region: RING domain"

Query Match 48.2%; Score 601; DB 8; Length 1168;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 160 ATGGGACCTTAAAGACAGTGGCCAAAGTGCCTGACCGTGGACACAGCCGAGCCACTGGGCA 219
 Db 1 ATGGGACCTTAAAGACAGTGGCCAAAGTGCCTGACCGTGGACACAGCCGAGCCACTGGGCA 60

QY 220 GCCGATATGATGCTCCACGACGAGACCGCTGTGAAACCCCGCTCTGTGGGCAAGCCCTGTCTTA 279
 Db 61 GCCGATATGATGCTCCACGACGAGCCGCTGTGAAACCCCGCTCTGTGGGCAAGCCCTGTCTTA 120

QY 280 GGCCTGACACCTGACAGAGCCTGGGACCAAGTGGATGGGAGATCTCTGGGACCAAGCTGGCG 339
 Db 121 GGCCTGACACCTGACAGAGCCTGGGACCAAGTGGATGGGAGATCTCTGGGACCAAGCTGGCG 180

QY 340 CCCCTGACAG 399
 Db 181 CCCCTGACAG 240

QY 400 TTCCCGGACATGGGCTCTGAGAGAGTGGCTGCTGCTGCTCTTATATGACTGGCCGCTGACT 459
 Db 241 TTCCCGGACATGGGCTCTGAGAGAGTGGCTGCTGCTGCTCTTATATGACTGGCCGCTGACT 300

QY 460 GCTGAGAGTGCACCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
 Db 301 GCTGAGAGTGCACCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

QY 520 AAGTGAAGTGTCTTCTTCTGCTATGAGAGGCTGACAGAGCTGGAAGCGCGGAGACGACCCC 579
 Db 361 AAGTGAAGTGTCTTCTTCTGCTATGAGAGGCTGACAGAGCTGGAAGCGCGGAGACGACCCC 420

QY 580 TGGACGAGAGATGCAAGTGGTTCCTCCAGTGTCACTCTGCTCCGGTCAAAAGAGAGA 639
 Db 421 TGGACGAGAGATGCAAGTGGTTCCTCCAGTGTCACTCTGCTCCGGTCAAAAGAGAGA 480

QY 640 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGAGGCTCTGGGACCAAGCCGCTG 699
 Db 481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGCTGAGGCTCTGGGACCAAGCCGCTG 540

QY 700 GAAGAACCAGGAAGACGACCCCTGTGGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
 Db 541 GAAGAACCAGGAAGACGACCCCTGTGGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY 760 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTCCACAGACCCAGAGAG 811
 Db 601 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAGTCCACAGACCCAGAGAG 652

Wed Apr 26 09:07:51 2006

us-09-762-577b-11.011.rge

Page 13

Search completed: April 22, 2006, 10:59:45
Job time : 6220 secs

THIS PAGE BLANK (USPTO)

Result No.	Score	Query Match	Length	DB	ID	Description
1	1228	98.6	1260	12	ADH89535	Adh89535 Human Liv
2	1228	98.6	1260	12	AEA316171	Aea316171 Human nuc
3	1228	98.6	1268	10	ACG72844	ACG72844 Human can
4	1228	98.6	1268	13	ADS71346	AdS71346 Human liv
5	1228	98.6	1376	4	AAE24856	AAE24856 Nucleotid
6	843	67.7	843	4	AAE24857	AAE24857 Nucleotid
7	793	63.6	1322	13	ACC72843	ACC72843 Human can
8	793	63.6	1322	13	ADS71344	AdS71344 Human liv
9	783	62.8	840	6	AAI42858	AAI42858 Survivin-
10	742	59.6	1337	3	AAE61210	AAE61210 DNA encod
11	742	59.6	1363	3	AAAI5007	AAAI5007 CDNA enco
12	742	59.6	1363	13	ADT88075	Adt88075 Human pro
13	638	51.2	858	12	ADQ25445	Adq25445 Human sof
14	601	48.2	1168	12	ADH89543	Adh89543 Human liv
15	593	47.6	672	6	AAI42857	AAI42857 Survivin-
16	593	47.6	723	6	AAI42856	AAI42856 Survivin-
17	532	42.7	1068	4	AAAI6364	AAAI6364 Human SBH
18	491	39.4	4810	12	ADH89542	Adh89542 Human liv
19	449	36.0	4490	12	ADQ21877	Adq21877 Human sof

20	447	35.9	769	4	AAD16355
21	439	35.2	676	12	AD021822
22	366	29.4	3782	5	AAS91553
23	311	25.0	615	4	AAH99228
24	310	24.9	614	5	AAS91350
25	268	21.5	444	5	AAS91551
26	262	21.0	399	14	AEA39948
27	204	16.4	204	6	AAL42854
28	204	13.5	226	11	ADJ31000
29	168	13.5	226	13	AD583077
30	168	11.3	141	6	AAL42855
31	122	9.8	404	5	AAE66630
32	94	7.5	200	10	ACA5561
33	94	7.5	200	11	ADJ31061
34	94	7.5	200	12	ADJ5541
35	94	7.5	200	13	AD583122
36	94	4.8	60	6	ABN40384
37	60	4.8	121	10	ADH9305
38	34	2.7	34	14	ADM7849
39	30	2.2	121	10	ADH9305
40	27	2.2	27	12	ADH89533
41	26	2.1	26	6	AAL42860
42	26	2.1	26	6	AAL42865
43	25	2.0	25	3	AAZ61213
44	25	2.0	25	3	AAZ61212
45	24	1.9	24	3	AAZ61215

Aa616358	Human SBH
Aa616358	Human scd
Aa915553	DNA encod
Aa919228	Human pro
Aa919520	DNA encod
Aa915551	DNA encod
Aa919481	Human M.
Aa112854	Survivin-
Aa131008	Human cdi
Aa2883075	Human ly
Aa2883075	Survivin-
Aa666690	Novel hum
Aa655618	Mouse si
Aa311061	Human cdi
Aa155414	Human po
Aa653128	Human ly
Aa9n0384	Human sp1
Aa9n3056	Human ge
Adw18491	Hybridize
Adh93505	Human ge
Adh98558	Human li
Aa142860	Survivin-
Aa142865	Survivin-
Aa616213	PCR prime
Aa616212	PCR prime
Aa616215	PCR prime

SQ Sequence 1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;
 Query Match 98.6%; Score 1228; DB 12; Length 1260;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 19 GGCAGGCGCTGTCCTATCCCTGCTGCTCCCGCAGGGTGGCCCGGGGGTCAAGAGCTTCAG 78
DB 33 GGCAGGCGCTGTCCTATCCCTGCTGCTCCCGCAGGGTGGCCCGGGGGTCAAGAGCTTCAG 92
QY 79 AAGGCGCAGCTGGGATATTCATGAGATTGAGCATCAGCCCCCATTTCTGCTGCAAACTGG 138
DB 93 AAGGCGCAGCTGGGATATTCATGAGATTGAGCATCAGCCCCCATTTCTGCTGCAAACTGG 152
QY 139 GTCAAGGCAAGTTCCTCTCATGGAGCTTAAGACAGTGCCTGCAACCTGTGA 198
DB 153 GTCAAGGCAAGTTCCTCTCATGGAGCTTAAGACAGTGCCTGCAACCTGTGA 212
QY 199 CCACAGCCGAGCACTGGGAGCCGGTATGTGCTCCACGGAGAGCGCTTGGACCCCGC 258
DB 213 CCACAGCCGAGCACTGGGAGCCGGTATGTGCTCCACGGAGAGCGCTTGGACCCCGC 272
QY 259 TCTCTGGGAGACCTGTCTTCTAGGCTTGAGACCTGACAGCCTTGGAGCACTGAGTGG 318
DB 273 TCTCTGGGAGACCTGTCTTCTAGGCTTGAGACCTGACAGCCTTGGAGCACTGAGTGG 332
QY 319 CAGATTCCTGGGCGCAGCTGCGGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 333 CAGATTCCTGGGCGCAGCTGCGGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
QY 379 ACCCTTGTTCAGAGGGGCGCTGCTTCCCGGAGTGGGCTTGAAGAGTGGCTGAGCTTC 438
DB 393 ACCCTTGTTCAGAGGGGCGCTGCTTCCCGGAGTGGGCTTGAAGAGTGGCTGAGCTTC 452
QY 439 TTCTATGACTGGCGGCTGACTGCTGAGTGGTGCACCCGAGCTGTGCTGCTCGCGCTTC 498
DB 453 TTCTATGACTGGCGGCTGACTGCTGAGTGGTGCACCCGAGCTGTGCTGCTCGCGCTTC 512
QY 499 TTCCACACAGGCCATCAGACCAAGTGAAGTCTTCTTGTGCTATGGGGGCGCTGAGAGC 558
DB 513 TTCCACACAGGCCATCAGACCAAGTGAAGTCTTCTTGTGCTATGGGGGCGCTGAGAGC 572
QY 559 TGAAGGCGGGAGACGACCCCTTGAAGAGCATGCCAAGTGTTCCTCCAGCTGTCACTTC 618
DB 573 TGAAGGCGGGAGACGACCCCTTGAAGAGCATGCCAAGTGTTCCTCCAGCTGTCACTTC 632
QY 619 CTGCTCCGCTCAAAAGAGAGACTTGTGCAAGTGTGAGAGAGACTCACTCCAGCTG 678
DB 633 CTGCTCCGCTCAAAAGAGAGACTTGTGCAAGTGTGAGAGAGACTCACTCCAGCTG 692
QY 679 CTGGGCTCTGGGAGACCCCTTGGAGAGAACCGGAGAGCGACCCCTTGGCCCTCCGCTC 738
DB 693 CTGGGCTCTGGGAGACCCCTTGGAGAGAACCGGAGAGCGACCCCTTGGCCCTCCGCTC 752
QY 739 CCTGCTCTGGGAGACCCCTTGAAGTGCACACCCAGAGAGAGAGTCCATCTGAAAGTGC 798
DB 753 CCTGCTCTGGGAGACCCCTTGAAGTGCACACCCAGAGAGAGAGTCCATCTGAAAGTGC 812
QY 799 CAGGAGCCGAGAGCCAGGAGATGTGAGAGCGACGCTGCGCGGCTGACAGAGAGAGAGC 858
DB 813 CAGGAGCCGAGAGCCAGGAGATGTGAGAGCGACGCTGCGCGGCTGACAGAGAGAGAGC 872
QY 859 TGCAGAGTGTGCTGAGACCGGCGGCTGTGCATCCGCTTTTGGTCCGCTGCGGCTGCTC 918
DB 873 TGCAGAGTGTGCTGAGACCGGCGGCTGTGCATCCGCTTTTGGTCCGCTGCGGCTGCTC 932
QY 919 TGTGCTGAGTGTGCTGAGACCGGCGGCTGTGCATCTGTCAGAGAGCCCGCTGCGAGC 978
DB 933 TGTGCTGAGTGTGCTGAGACCGGCGGCTGTGCATCTGTCAGAGAGCCCGCTGCGAGC 992
QY 979 CGCGTGCAGACCTTCTGCTTCTTGAAGCCAGGTCAGGTCAGGTCAGGTCAGAGT 1038
DB 993 CGCGTGCAGACCTTCTGCTTCTTGAAGCCAGGTCAGGTCAGGTCAGGTCAGAGT 1052
  
```

```

QY 1039 GGGCTCCCTGCGCCCTCTGCTGCTTCTGAGCTGTGTTCTGGGCGCTGTGAGATGGCAG 1098
DB 1053 GGGCTCCCTGCGCCCTCTGCTGCTTCTGAGCTGTGTTCTGGGCGCTGTGAGATGGCAG 1112
QY 1099 AGCTGTGTGCTTCCAGACCTGACACGACCCGATTCCTCCGACACCCGCGAGTGAAGA 1158
DB 1113 AGCTGTGTGCTTCCAGACCTGACACGACCCGATTCCTCCGACACCCGCGAGTGAAGA 1172
QY 1159 AGGAGCCCTTGTGCTTGGGCGGATGTGCTTAAGTATCCTGTTGATGCTTGAAT 1218
DB 1173 AGGAGCCCTTGTGCTTGGGCGGATGTGCTTAAGTATCCTGTTGATGCTTGAAT 1232
QY 1219 AGAATTAAGTGGGTTTCTCCCTGAGAGT 1246
DB 1233 AGAATTAAGTGGGTTTCTCCCTGAGAGT 1260
  
```

RESULT 2
 AEA36171
 ID AEA36171 standard; DNA; 1260 BP.
 AC AEA36171;
 DT 25-AUG-2005 (first entry)
 XX
 DE Human nucleic acid sequence #103.
 XX
 KW Screening; gene expression; colorectal tumor; colitis; Crohn's disease;
 KW irritable bowel syndrome; gastrointestinal disease; cytostatic;
 KW gastrointestinal-gen.; antiinflammatory; ds.
 OS Homo sapiens.
 XX
 PN M02005054507-A2.
 XX
 PD 16-JUN-2005.
 XX
 PF 03-DEC-2004; 2004MO-GB005078.
 XX
 PR 04-DEC-2003; 2003GB-00028048.
 XX
 PA (VUSH-) UNIV SHEFFIELD.
 PI Corfe B, Chirakkal H;
 XX
 DR WPI; 2005-435407/44.
 XX
 PT Screening for nucleic acid molecules exhibiting altered expression in
 PT cells grown in the presence of butyrate, and detection of the nucleic
 PT acid molecules or the encoded polypeptides in diagnosing colorectal
 cancer.
 XX
 PS Disclosure; Page 143; 266bp; English.
 XX
 CC The invention relates to a method of screening for nucleic acid molecules
 CC that show altered expression in a first cell sample comprising comparing
 CC the gene expression profile of the sample with that of a second reference
 CC sample, where the first sample has been grown in the presence of butyrate
 CC or a related carbon source from which butyrate is directly or indirectly
 CC derived, but the reference sample has not. The invention also relates to
 CC a method of detecting at least one nucleic acid molecule associated with
 CC the initiation and/or progression of colorectal cancer in an animal,
 CC comprising providing a biological sample comprising at least one cell to
 CC be tested, contacting the sample with a ligand (preferably a hybridizing
 CC nucleic acid molecule) which binds to at least one nucleic acid and
 CC detecting the presence of at least one molecule in the sample, a method
 CC and/or progression of colorectal cancer in an animal comprising providing
 CC a biological sample comprising at least one cell to be tested, contacting
 CC the sample with at least one ligand that specifically binds at least one
 CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising
 CC an amino acid sequence which varies by the addition, deletion or

PI Afar D, Aziz N, Gish KC, Heyezi PA, Mack DH, Wilson KE;
PI Zlonick A;
XX
XX MPI: 2003-354600/33.
DR P-PSDB; ABR58693.
XX

PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
XX

PS Claim 8; Page 725-726; 767pp; English.

XX
XX The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1033 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
XX pathologies
XX

SQ Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;

Query Match 98.6%; Score 1228; DB 10; Length 1268;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGCAGGCTTGCTGCTATCCCTGCTGCCAGAGGTGGGCGCGGGGTCAGAGCTCCAG 78
Db 33 GGCAGGCTTGCTGCTATCCCTGCTGCCAGAGGTGGGCGCGGGGTCAGAGCTCCAG 92
QY 79 AAGGGGACGCTGGGCAATTTCTAGATTGGCAATGAGCCCCCATTTCTGCTGCACAACTG 138
Db 93 AAGGGGACGCTGGGCAATTTCTAGATTGGCAATGAGCCCCCATTTCTGCTGCACAACTG 152
QY 139 GTCAGAGCAGTGTTCCTCCATGGGAGCTTAAAGCAGTGGCCAAATGCTGTCACCTGGA 198
Db 153 GTCAGAGCAGTGTTCCTCCATGGGAGCTTAAAGCAGTGGCCAAATGCTGTCACCTGGA 212
QY 199 CCACAGCCGAGCCACTGGGACCGGATGATGTTCCACGACGAGAGCGCTGTGACCCCGC 258
Db 213 CCACAGCCGAGCCACTGGGACCGGATGATGTTCCACGACGAGAGCGCTGTGACCCCGC 272
QY 259 TCTCTGGGAGCGCTGTCTTAGGCTTGACACCTTGCAGAGCTTGAGACCTGTGATGG 318
Db 273 TCTCTGGGAGCGCTGTCTTAGGCTTGAGACCTTGCAGAGCTTGAGACCTGTGATGG 332
QY 319 CAGATCTTGGGCGCAGCTGGGCGCTTGA CAGAGAGAGAGAGAGAGGCGCGGGGCC 378
Db 333 CAGATCTTGGGCGCAGCTGGGCGCTTGA CAGAGAGAGAGAGAGAGGCGCGGGGCC 392
QY 379 ACCCTGTCCAGGGGCGCTGCTTCCCGGCAATGGGCTTGAAGATTGCGTGTGACCTCC 438
Db 393 ACCCTGTCCAGGGGCGCTGCTTCCCGGCAATGGGCTTGAAGATTGCGTGTGACCTCC 452
QY 439 TTCTATGACTGGCCGCTGACTGTAGAGTGCACCCGAGCGTGGCTGCGCGGTTTC 498
Db 453 TTCTATGACTGGCCGCTGACTGTAGAGTGCACCCGAGCGTGGCTGCGCGGTTTC 512
QY 499 TTCCACAGAGGCATCAGAGCAAGGTGAGTGTCTTTCTGCTATGGGGGCGCTGACAGC 558

Db 513 TTCCACAGAGGCATCAGAGCAAGGTGAGTGTCTTTCTGCTATGGGGGCGCTGACAGC 572
QY 559 TGGAAACCGGGGAGCAGACCCCTTGACGAGAGATGCCAATGTTGCCAGCTGTCACTTC 618
Db 573 TGGAAACCGGGGAGCAGACCCCTTGACGAGAGATGCCAATGTTGCCAGCTGTCACTTC 632
QY 619 CTGCTCCGGATCAAAAGAGAGACTTTGTCCACAGTGTGCAGAGACTCACTCCACCTG 678
Db 633 CTGCTCCGGATCAAAAGAGAGACTTTGTCCACAGTGTGCAGAGACTCACTCCACCTG 692
QY 679 CTGGCTCTTGGAGCCCGTGGAAAGAACCGGAAACCGAGCCCTGTGAGCCCTCCGTC 738
Db 693 CTGGCTCTTGGAGCCCGTGGAAAGAACCGGAAACCGAGCCCTGTGAGCCCTCCGTC 752
QY 739 CTTGCTCTTGGAGTACCTTGAGAGTCCCAACCCGAGAGAGAGTCCAGTGTAAAGTGC 798
Db 753 CTTGCTCTTGGAGTACCTTGAGAGTCCCAACCCGAGAGAGAGTCCAGTGTAAAGTGC 812
QY 799 CAGAGCCAGAGAGCCAGAGATGTGAGAGCCAGCTGCGGCGTGCAGAGAGAGAGAGC 858
Db 813 CAGAGCCAGAGAGCCAGAGATGTGAGAGCCAGCTGCGGCGTGCAGAGAGAGAGAGC 872
QY 859 TGCAGAGTGTGCTTGCAGCCGCGCTGTCCATGTCTTTGTGCGCGTGCACCTGCTC 918
Db 873 TGCAGAGTGTGCTTGCAGCCGCGCTGTCCATGTCTTTGTGCGCGTGCACCTGCTC 932
QY 919 TGTGCTAGTGTGCCCCCGGCTGCACTGTGCCCCATCTGCAGAGCCCCCTGCCAGC 978
Db 933 TGTGCTAGTGTGCCCCCGGCTGCACTGTGCCCCATCTGCAGAGCCCCCTGCCAGC 992
QY 979 CGCGTGACACCTTCTCTGTCTTAGGCGAGTGCATGCGCGGCGAGTGGCTGCAGAT 1038
Db 993 CGCGTGACACCTTCTCTGTCTTAGGCGAGTGCATGCGCGGCGAGTGGCTGCAGAT 1052
QY 1039 GGGCTCCCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098
Db 1053 GGGCTCCCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
QY 1099 AGCTGTGCTCATTCAGACACTGACCAAGCCCTGATTTCCCGAACCAAGCGGAGTGGAGA 1158
Db 1113 AGCTGTGCTCATTCAGACACTGACCAAGCCCTGATTTCCCGAACCAAGCGGAGTGGAGA 1172
QY 1159 AGGAGGCGCTGTGCTGCGCGGAGGAGATGGCTTAACCTGTTTGGATGCTTTGAAT 1218
Db 1173 AGGAGGCGCTGTGCTGCGCGGAGGAGATGGCTTAACCTGTTTGGATGCTTTGAAT 1232
QY 1219 AGAATTAAGTGAGTGTTCCTCTGAGAGT 1246
Db 1233 AGAATTAAGTGAGTGTTCCTCTGAGAGT 1260

RESULT 4
AD571346
ID AD571346 standard; DNA; 1268 BP.
XX
XX AD571346;
AC
XX
XX 16-DEC-2004 (first entry)
DT
XX
XX Human livin beta splice variant DNA.
DE
XX
XX Immune response; cancer-associated inhibitor of Apoptosis-family protein;
KW IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;
KW human; livin beta; gene; de; immunostimulant; cytosolic.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
CDS 174..1016
FT /tag=a
FT /product="Human livin beta splice variant protein"
XX
PN US2004192631-A1.

```

XX 30-SEP-2004.
XX
XX 24-MAR-2004; 2004US-00807897.
XX
XX 24-MAR-2003; 2003US-0457009P.
XX
XX (XIAN/) XIANG R.
XX (ZHOU/) ZHOU H.
XX (REIS/) REISFELD R A.
XX
XX Xiang R, Zhou H, Reisfeld RA;
XX
XX MPI, 2004-689881/67.
XX P-PSDB; ADS71347.
XX DR REFSEQ; NM_022161.
XX
XX New DNA vaccine comprising a cancer-associated Inhibitor of Apoptosis-
XX family protein immunoreactive gene product, useful for eliciting an immune
XX response against cancer.
XX
XX Claim 26; SEQ ID NO 28; 84bp; English.
XX
XX The present invention relates to a DNA vaccine effective for eliciting an
XX immune response against cancer cells which comprises a DNA construct
XX operably encoding at least one cancer-associated inhibitor of Apoptosis-
XX family protein (IAP-family protein) and at least one immunoreactive gene
XX product in a pharmaceutical carrier. The invention is useful for treating
XX cancer such as lung cancer, colorectal cancer and melanoma. The present
XX sequence is the human livin beta splice variant DNA.
XX
XX Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;
XX
XX Query Match 98.6%; Score 1228; DB 13; Length 1268;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 19 GGCAGGCTGTGCTTATCCCTGCTGTCCTCCAGGCTGGGCGCGGGCTCAGAGCTCCAG 78
XX 33 GGCAGGCTGTGCTTATCCCTGCTGTCCTCCAGGCTGGGCGCGGGCTCAGAGCTCCAG 92
XX
XX 79 AAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 138
XX 93 AAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 152
XX
XX 139 GTCAAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 198
XX 153 GTCAAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 212
XX
XX 199 CCACAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 258
XX 213 CCACAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 272
XX
XX 259 TCTTGGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 318
XX 273 TCTTGGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 332
XX
XX 319 CAGATCTGGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 378
XX 333 CAGATCTGGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 392
XX
XX 379 ACCTTGTCCAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 438
XX 393 ACCTTGTCCAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 452
XX
XX 439 TTCTATGACTGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 498
XX 453 TTCTATGACTGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 512
XX
XX 499 TTCCACACAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 558
XX 513 TTCCACACAGGCGCAGCTGGGATATTCGAGATTGGCCATCAGGCCCATTTCTGCTGCAAACTG 572

```

```

QY 559 TGAAGCGCGGGGAGCAGACCCCTTGGACGAGCATGCGCAAGTGTTCCTCCAGCTGTCACTTC 618
DB 573 TGAAGCGCGGGGAGCAGACCCCTTGGACGAGCATGCGCAAGTGTTCCTCCAGCTGTCACTTC 632
QY 619 CTGCTCCGCGTCAAAAGGAGAGACTTGTTCACAGTGTGAGAGAGTCACTCCAGCTG 678
DB 633 CTGCTCCGCGTCAAAAGGAGAGACTTGTTCACAGTGTGAGAGAGTCACTCCAGCTG 692
QY 679 CTGCGCTCTTGGGAGCCCGTGGGAAAGAACCGGAGACCGCCCTGTGTGCGCCCTGCTG 738
DB 693 CTGCGCTCTTGGGAGCCCGTGGGAAAGAACCGGAGACCGCCCTGTGTGCGCCCTGCTG 752
QY 739 CTGCGCTCTTGGGAGCCCGTGGGAAAGAACCGGAGACCGCCCTGTGTGCGCCCTGCTG 798
DB 753 CTGCGCTCTTGGGAGCCCGTGGGAAAGAACCGGAGACCGCCCTGTGTGCGCCCTGCTG 812
QY 799 CAGAGCGCAGAGCGAGGATGTGAGAGCGGAGCTGGCGGCGGCTGCGAGAGAGAGAGAG 858
DB 813 CAGAGCGCAGAGCGAGGATGTGAGAGCGGAGCTGGCGGCGGCTGCGAGAGAGAGAGAG 872
QY 859 TGAAGGCTGTGCTGAGACCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 918
DB 873 TGAAGGCTGTGCTGAGACCGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 932
QY 919 TGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 978
DB 933 TGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 992
QY 979 CGCGTGGCGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1038
DB 993 CGCGTGGCGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1052
QY 1039 GGGCTCCCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1098
DB 1053 GGGCTCCCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1112
QY 1099 AGCTGTGTTCATTCAGACATGACAGCTGAGTTCCTCCAGCACCGCCGAGGTGAGAG 1158
DB 1113 AGCTGTGTTCATTCAGACATGACAGCTGAGTTCCTCCAGCACCGCCGAGGTGAGAG 1172
QY 1159 AGAGGCGCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1218
DB 1173 AGAGGCGCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1232
QY 1219 AGAATAAAGTGGGTTTCTCTGAGAGT 1246
DB 1233 AGAATAAAGTGGGTTTCTCTGAGAGT 1260

```

RESULT 5
 AAF24856
 ID AAF24856 standard; cDNA; 1376 BP.
 AC AAF24856;
 XX
 AC 20-APR-2001 (first entry)
 DT
 XX
 XX Nucleotide sequence of an apoptosis inhibitor designated livin.
 DE
 XX
 XX Livin; apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;
 KW melanoma; Alzheimer's disease; Parkinson's disease; ss.
 OS
 XX Homo sapiens.
 OS
 XX
 FT Key Location/Qualifiers
 CDS 211..1053
 FT /*tag= a
 FT /product= "livin"
 XX
 XX MO200077201-A1.
 XX
 XX 21-DEC-2000.
 XX

comprising the vector: (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies

Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other;

```
Query Match      63.6%; Score 793; DB 10; Length 1322;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	GGCAGAGCCTGGTGGCTATTCCTCGTGTCTCCAGAGGTGGGCCCGGGGGGTCCAGAGGCTCCAG	78
Db	33	GGCAGAGCCTGGTGGCTATTCCTCGTGTCTCCAGAGGTGGGCCCGGGGGGTCCAGAGGCTCCAG	92
QY	79	AAGGCGCAGCTGGGCAATTCCTGAGATTGGCATCGAGCCGCCATTTCTGTGCAAACTTG	137
Db	93	AAGGCGCAGCTGGGCAATTCCTGAGATTGGCATCGAGCCGCCATTTCTGTGCAAACTTG	151
QY	139	GTCAAGCCAGTGTTCCTCCATGGGACCTTAAAGCAGTGGCCAGTGGCTGACCCGTGGA	198
Db	153	GTCAAGCCAGTGTTCCTCCATGGGACCTTAAAGCAGTGGCCAGTGGCTGACCCGTGGA	212
QY	159	CCACAGCCGAGACCTAGGGCAGCCGGTGTATGTCTCCAGCAGAGCCGTGTGAACTCCGC	258
Db	213	CCACAGCCGAGACCTAGGGCAGCCGGTGTATGTCTCCAGCAGAGCCGTGTGAACTCCGC	272
QY	259	TCTCGGGCAGCCCTGTCTTAGGCTTGGACACTGTGAGCCCTGGGACCAAGTGTATGG	318
Db	273	TCTCGGGCAGCCCTGTCTTAGGCTTGGACACTGTGAGCCCTGGGACCAAGTGTATGG	332
QY	319	CAGATCCTGGCCAGCTGCAGGCCCTTGACAGAGAGAGAAAGAGAGAGAGGCGCGGGGCC	378
Db	333	CAGATCCTGGCCAGCTGCAGGCCCTTGACAGAGAGAGAGAAAGAGAGAGAGGCGCGGGGCC	392
QY	379	ACCTTGTTCAGAGGGGCGCTTGCTCCCGGCATGGGCTCTGAGAGATTGCGTGTGACCTTC	438
Db	393	ACCTTGTTCAGAGGGGCGCTTGCTCCCGGCATGGGCTCTGAGAGATTGCGTGTGACCTTC	452
QY	439	TTCTATATACGTGGCCGCTGACTGTGAGGTGCCAACCAGACTGTGGCTGTGCGGCTTC	498
Db	453	TTCTATATACGTGGCCGCTGACTGTGAGGTGCCAACCAGACTGTGGCTGTGCGGCTTC	512
QY	499	TTTCACACAGGCGCATCGAGCAAGGTGAGGTCTTCTCTGCTATGGGGCGCTTCAGAGC	558
Db	513	TTTCACACAGGCGCATCGAGCAAGGTGAGGTCTTCTCTGCTATGGGGCGCTTCAGAGC	572
QY	559	TGGAAGCGCGGGGACGACCCCTTGACAGGACATGSCAAAGTGTTCGCCAGCTGTCAATTTC	618
Db	573	TGGAAGCGCGGGGACGACCCCTTGACAGGACATGSCAAAGTGTTCGCCAGCTGTCAATTTC	632
QY	619	CTGCTCCGGTCAAAAGGAAGAGCTTTGTGCCAGTGTGCAAGAGACTCACTCCAGCTG	678
Db	633	CTGCTCCGGTCAAAAGGAAGAGCTTTGTGCCAGTGTGCAAGAGACTCACTCCAGCTG	692
QY	679	CTGGGCTCTGGAGCCCGTGGAGAAACCGAGAACGAGGCCCTGTGGGCCCTCCCTCCGTC	738
Db	693	CTGGGCTCTGGAGCCCGTGGAGAAACCGAGAACGAGGCCCTGTGGGCCCTCCCTCCGTC	752
QY	739	CTGTGCTCTGGAGTACCTTGAGCTGCCACATCCAGAGAGAGTCTCAGTCTGAAAGTGCC	798
Db	753	CTGTGCTCTGGAGTACCTTGAGCTGCCACATCCAGAGAGAGTCTCAGTCTGAAAGTGCC	812
QY	799	CAGAGCCAGAG	811

Db		813	CAGAGGCCAGGAG	825
		RESULT 8		
		AD571344		
		ID	AD571344 standard; DNA; 1322 BP.	
		XX		
		AC	AD571344;	
		XX		
		DT	16-DEC-2004 (first entry)	
		XX		
		DE	Human livin alpha splice variant DNA.	
		KW		
		KM	Immune response; cancer-associated inhibitor of Apoptosis-family protein IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma; human; livin alpha; gene; ds; immunostimulant; cytosolic.	
		OS	Homo sapiens.	
		XX		
		FH		
		FT	Location/Qualifiers	
		CDS	174..1070	
		FT	/+tag= a	
		FT	/product= "Human livin alpha splice variant protein"	
		XX		
		FN	US2004192631-A1.	
		PD		
		XX	30-SEP-2004.	
		XX		
		PX	24-MAR-2004; 2004US-00807897.	
		PR		
		XX	24-MAR-2003; 2003US-0457009P.	
		PA	(XIAN/) XIANG R.	
		PA	(ZHOU/) ZHOU H.	
		PA	(REIS/) REISFELD R. A.	
		XX		
		PI	Xiang R, Zhou H, Reisfeld RA;	
		XX		
		DR	WPI: 2004-689881/67.	
		DR	P-PSDB: AD571345.	
		DR	REFSEQ: NM_139317.	
		XX		
		PT	New DNA vaccine comprising a cancer-associated inhibitor of Apoptosis-	
		PT	family protein immunosensitive gene product, useful for eliciting an immune	
		PT	response against cancer.	
		XX		
		PS	Claim 26; SEQ ID NO 26; 84bp; English.	
		XX		
		CC	The present invention relates to a DNA vaccine effective for eliciting an	
		CC	immune response against cancer cells which comprises a DNA construct	
		CC	operably encoding at least one cancer-associated inhibitor of Apoptosis-	
		CC	famly protein (IAP-family protein) and at least one immunosensitive gene	
		CC	product in a pharmaceutical carrier. The invention is useful for treating	
		CC	cancer such as lung cancer, colorectal cancer and melanoma. The present	
		CC	sequence is the human livin alpha splice variant DNA.	
		XX		
		XX		
		SQ	Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other:	
		Query Match	63.6%; Score 793; DB 13; Length 1322;	
		Best Local Similarity	100.0%; Pred. No. 0;	
		Matches 793; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
		19	GCGAGGCCTGTGGCTATCCTCGTGTGTCAGGAGGTTGGGCCCCGGGGGTCAAGAAGCTCCAG	78
		Db	33 GCGAGGCCTGTGGCTATCCTCGTGTGTCAGGAGGTTGGGCCCCGGGGGTCAAGAAGCTCCAG	92
		79	AAGGGCCAGACTGGCATATTCTTGAGATTGGCATCAGCCCCTTCTGCTGCAAACTG	138
		Db	93 AAGGGCCAGACTGGCATATTCTTGAGATTGGCATCAGCCCCTTCTGCTGCAAACTG	152
		139	GTCAGAGCCAGTGTTCCTTCATGGAGCTTAAGACAGTGCACAAGTGCCTGCACCGTGA	198
		Db	153 GTCAGAGCCAGTGTTCCTTCATGGAGCTTAAGACAGTGCACAAGTGCCTGCACCGTGA	212

```
QY 199 CCACAGCCGAGCCACTGCGGCAAGCCCGGTATGATGATCCACGACGAGACCGCTGTGAGACCCCGC 258
DB 213 CCACAGCCGAGCCACTGCGGCAAGCCCGGTATGATGATCCACGACGAGACCGCTGTGAGACCCCGC 272
QY 259 TCTGTGGGCAAGCCGCTGCTAGAGCTTGAGACACTCTGACAGAGCTGGGACCAAGTGTGATGG 318
DB 273 TCTGTGGGCAAGCCGCTGCTAGAGCTTGAGACACTCTGACAGAGCTGGGACCAAGTGTGATGG 332
QY 319 CAGATCTGGGCGCAGCTGCGGCGCTGACAGAGAGAAAGAGAGAGAGGCGCGCGGGCC 378
DB 333 CAGATCTGGGCGCAGCTGCGGCGCTGACAGAGAGAAAGAGAGAGAGGCGCGGGCC 392
QY 379 ACCCTGTCCAGGGGCGCTGCTTCCCGGCAATGGCTCTGAGAGATGGCTGTGAGCTTC 438
DB 393 ACCCTGTCCAGGGGCGCTGCTTCCCGGCAATGGCTCTGAGAGATGGCTGTGAGCTTC 452
QY 439 TTCTATGACTGGCGCTGACTGCTGAGGTGCGACCCGAGCTGCTGCTGCGCGGCTTC 498
DB 453 TTCTATGACTGGCGCTGACTGCTGAGGTGCGACCCGAGCTGCTGCTGCGCGGCTTC 512
QY 499 TTCCACACAGGCGCATCAGAGACAGGTGAGGTGCTTCTTCTGCTATGAGGGCGCTGACAGC 558
DB 513 TTCCACACAGGCGCATCAGAGACAGGTGAGGTGCTTCTTCTGCTATGAGGGCGCTGACAGC 572
QY 559 TGGAGAGCGCGGGGAGACGACCCCTGAGCGAGCATGCGCAAGTGTTCCTCCAGCTGTCAATTTC 618
DB 573 TGGAGAGCGCGGGGAGACGACCCCTGAGCGAGCATGCGCAAGTGTTCCTCCAGCTGTCAATTTC 632
QY 619 CTGCTCCGCTGAAAAAGAGAGACTTGTTCACAGTGTGACGAGAGACTCACTCCAGCTG 678
DB 633 CTGCTCCGCTGAAAAAGAGAGACTTGTTCACAGTGTGACGAGAGACTCACTCCAGCTG 692
QY 679 CTGGGCTCTTGGGACCCGCTGGAGAACCGGAGACGCGAGCCCTGTGGCCCTCCGCTC 738
DB 693 CTGGGCTCTTGGGACCCGCTGGAGAACCGGAGACGCGAGCCCTGTGGCCCTCCGCTC 752
QY 739 CCTGCTCTTGGGATACCTTGAGCTGCGCCACCCGAGAGAGAGTTCAGTCTGAAGTCC 798
DB 753 CCTGCTCTTGGGATACCTTGAGCTGCGCCACCCGAGAGAGAGTTCAGTCTGAAGTCC 812
QY 799 CAGAGCCAGGAG 811
DB 813 CAGAGCCAGGAG 825

RESULT 9
AAL42858
ID AAL42858 standard; DNA; 840 BP.
AC AAL42858;
XX
XX
DT 05-AUG-2002 (first entry)
XX
XX DE Survivin-like protein coding sequence 5.
XX
XX KM Survivin-like protein; diagnosis; screening; cancer; gene; ds;
XX KM apoptosis abnormality; gene therapy.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT 1..840
XX FT /*tag= a
XX FT /partial
XX FT /product= "Survivin-like protein 5"
XX FT /note= "No stop codon is given"
XX
XX PN MO200233071-A1.
XX
XX 25-APR-2002.
XX
XX 16-OCT-2001; 2001WO-JP009071.
```

```
XX
XX 17-OCT-2000; 2000JP-00316721.
XX 20-DEC-2000; 2000JP-00386809.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Tanaka H, Kaieda I;
XX
XX WPI; 2002-435536/46.
XX P-PSDB; AAO14947.
XX
XX Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
XX PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
XX compounds for treating various cancers and apoptosis abnormality.
XX
XX PS Disclosure; Page 122; 136pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of survivin-
XX CC like proteins. The survivin-like DNA and protein sequences are useful in
XX CC diagnostics and screening compounds for treating various cancers and
XX CC apoptosis abnormality, including gene therapy. The present DNA sequence
XX CC encodes a survivin-like protein of the invention
XX
XX SQ Sequence 840 BP; 136 A; 272 C; 287 G; 144 T; 0 U; 1 Other;

Query Match 62.8%; Score 783; DB 6; Length 840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 CCTAAGACAGTGCAGAGTGCCTGACCGTGGACACAGCCGACCTGCTGAGGCTG 225
DB 7 CCTAAGACAGTGCAGAGTGCCTGACCGTGGACACAGCCGACCTGCTGAGGCTG 66
QY 226 GATGATCCCAAGCAGAGGCGCTGTGAGACCCCGCTCTGTGGGCAAGCCCTGTCTGAGGCTG 285
DB 67 GATGATCCCAAGCAGAGGCGCTGTGAGACCCCGCTCTGTGGGCAAGCCCTGTCTGAGGCTG 126
QY 286 GACACTCTGACAGGCTTGGAGACCACTGTGATGGAGATCTTGTGGGCAAGCTTGGGCGCTG 345
DB 127 GACACTCTGACAGGCTTGGAGACCACTGTGATGGAGATCTTGTGGGCAAGCTTGGGCGCTG 186
QY 346 ACAGAGGAGAGAGAGAGAGAGGCGCGGCGCACTTGTTCAGAGGGGCGCTTGTCC 405
DB 187 ACAGAGGAGAGAGAGAGAGAGGCGCGGCGCACTTGTTCAGAGGGGCGCTTGTCC 246
QY 406 GGCATGGGCTCTGAGAGATGTGCGTGGCTCTCTCTATGACTGAGCGCTGACTGCTGAG 465
DB 247 GGCATGGGCTCTGAGAGATGTGCGTGGCTCTCTCTATGACTGAGCGCTGACTGCTGAG 306
QY 466 GTGCCACCCGAGCTGTGAGCTGTGCGGCTTCTTCACACAGGCCATCAGAGCAAGGTG 525
DB 307 GTGCCACCCGAGCTGTGAGCTGTGCGGCTTCTTCACACAGGCCATCAGAGCAAGGTG 366
QY 526 AGGTGCTTCTTGTGATGGGGGCGCTGACAGCTGAGAGGCGGGGAGACCCCTGAGC 585
DB 367 AGGTGCTTCTTGTGATGGGGGCGCTGACAGCTGAGAGGCGGGGAGACCCCTGAGC 426
QY 586 GAGCATGCAAGTGTGTCCCAAGCTGTCACTTCCGCTCCGCTCAAAAGAGAGACTTT 645
DB 427 GAGCATGCAAGTGTGTCCCAAGCTGTCACTTCCGCTCCGCTCAAAAGAGAGACTTT 486
QY 646 GTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTGTGAGGACCCGTGGAGAA 705
DB 487 GTCCACAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTGTGAGGACCCGTGGAGAA 546
QY 706 CCGGAGAGCAGAGCCCTGTGAGCCCTCCGCTCCGCTCTGAGGTACCTGTGAGCTGCC 765
DB 547 CCGGAGAGCAGAGCCCTGTGAGCCCTCCGCTCCGCTCTGAGGTACCTGTGAGCTGCC 606
QY 766 ACAACCCAGAGAGAGTGTCAAGTGTAAAGTGTCCAGAGGCAAGAGCCAGAGGATGTGAG 825
DB 607 ACAACCCAGAGAGAGTGTCAAGTGTAAAGTGTCCAGAGGCAAGAGCCAGAGGATGTGAG 666
```


QY	826	GCGAGCTGCGCGCGCTCCAGAGAGAGAGACGTGCAAGTGTGCTCCGACCGCGCGTG	885					
Db	667	GCGAGCTGCGCGCGCTCCAGAGAGAGAGACGTGCAAGTGTGCTCCGACCGCGCGTG	726					
QY	886	TCGATCGCTTGTGCGCGCGCACCTGATCTGTGCTGATGATGCCCCCGGCTTCAG	945					
Db	727	TCGATCGCTTGTGCGCGCGCACCTGATCTGTGCTGATGATGCCCCCGGCTTCAG	786					
QY	946	CTGAGCCCGATCTGAGAGCGCCCGTCGAGCGCGCGTGGCACCCTTCTGTCC	999					
Db	787	CTGAGCCCGATCTGAGAGCGCCCGTCGAGCGCGCGTGGCACCCTTCTGTCC	840					
RESULT 10								
ID	AA61210	standard; DNA, 1337 BP.						
XX	AA61210,							
AC	30-MAY-2000	(first entry)						
DX	DNA encoding a human inhibitor of apoptosis protein (HIAP3).							
XX	Human, inhibitor of apoptosis protein; HIAP3; apoptosis; cancer;							
KW	chronic viral infection; neurodegenerative disorder;							
KW	chronic heart failure; dysfunctional immune response; ss.							
XX	Homo sapiens.							
OS								
XX								
FT	Key	Location/Qualifiers						
FT	CDS	170..1066						
FT	/tag= a							
FT	/product= "human inhibitor of apoptosis protein"							
PN	WO200008144-A1.							
XX								
PD	17-FEB-2000.							
XX								
PF	23-JUL-1999;	99WO-EP005471.						
XX								
PR	31-JUL-1998;	98US-00127928.						
XX								
PA	(SCHD) SCHERING AG.							
XX								
PI	Deng G, Lin J, Morseer MJ;							
DR	MPI, 2000-195573/17.							
DR	F-PSDB; AAY69182.							
XX								
PT	New DNA encoding human inhibitor-of-apoptosis protein, useful for							
PT	regulation of apoptosis.							
XX								
PS	Claim 10; Fig 1; 57pp; English.							
XX								
CC	The present sequence encodes a human inhibitor of apoptosis protein,							
CC	designated HIAP3. The protein is characterised by structural features							
CC	common to the inhibitor of apoptosis protein family. The HIAP3							
CC	polypeptides can be used for the treatment of a disease state in a human							
CC	patient, which is associated with inappropriate apoptosis and the patient							
CC	is in need of increased levels of the polypeptide. Ribozymes, which							
CC	target RNA encoding the polypeptide coding sequences, are useful for							
CC	decreasing levels of the polypeptide for treatment of inappropriate							
CC	apoptosis. Antisense nucleotide sequences are also useful for decreasing							
CC	levels of the polypeptide. Regulation of inhibitor of apoptosis proteins							
CC	may be useful in treatment of cancer, chronic viral infections,							
CC	neurodegenerative disorders, chronic heart failure and dysfunctional							
XX	immune response							
XX								
SO	Sequence 1337 BP; 231 A; 413 C; 445 G; 248 T; 0 U; 0 Other;							
Query Match								
Best Local Similarity 59.6%; Score 742; DB 3; Length 1337;								
Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;								

Oy		19	GAGAGGCTGTGGCCATATCCCTGCTGTGCCACGGGTGGGCCCCCGGGGGTCAAGAGCTTCAG	78			
Db		29	GGAAGGCTGTGCCTCATATCCTGTGTCTCCACGGGTGGGGCCCGGGGGTCAAGAGCTTCAG	88			
Oy		79	AAGGGCACAGCTGGGCATATTCTTGAGATTGGCCATCAGCCCCCATTTCTGTGTCAAACCTTG	13			
Db		89	AAGGGCACAGCTGGGCATATTCTTGAGATTGGGCATCAGCCCCCATTTCTGTGTCAAACCTTG	14			
Oy		139	GTCAAGAGCCAGGTTCCTCCTCATATGGACCTTAAGA CAGTGC CAAGTGCCTGCACCCTGGA	19			
Db		149	GTCAAGAGCCAGGTTCCTCCTCATATGGACCTTAAGA CAGTGC CAAGTGCCTGCACCCTGGA	20			
Oy		199	CCACAGCCGAGCCA CTGGGCAGCCGGTGTGTCCTCCACGAGGAGGGCTGTGGACCCCGC	25			
Db		209	CCACAGCCGAGCCA CTGGGCAGCCGGTGTGTCCTCCACGAGGAGGGCTGTGGACCCCGC	26			
Oy		259	TCTCTGGGCAAGCCTGTGCTTAAGGCTTGAGACA CTGGAAGACCTGGGACCAAGTGA TGGG	31			
Db		269	TCTCTGGGCAAGCCTGTGCTTAAGGCTTGAGACA CTGGAAGACCTGGGACCAAGTGA TGGG	32			
Oy		319	CAGATCCTGGGSCA GCTGCGGCCCCTCTACAGAGAGAAAGAGAGAGAGGGCCCGGGCC	37			
Db		329	CAGATCCTGGGSCA GCTGCGGCCCCTCTACAGAGAGAAAGAGAGAGAGGGCCCGGGCC	38			
Oy		379	ACCTTGTCAAGGGGGCCTGCTTTCCCGGACATGGGCTCTGAGAGATTGGCTGTGACTCC	43			
Db		389	ACCTTGTCAAGGGGGCCTGCTTTCCCGGACATGGGCTCTGAGAGATTGGCTGTGACTCC	44			
Oy		439	TTCTATGACTGGCCGCTGA CTGCTGAGAGTGCCACCCGAGCTGTGGCTGTGCGCGCTTC	49			
Db		449	TTCTATGACTGGCCGCTGA CTGCTGAGAGTGCCACCCGAGCTGTGGCTGTGCGCGCTTC	50			
Oy		489	TTCCACAAGGCCATCA GAACAAGGTAGGTCTTTCTGCTATGGGGGCTGCAAGAC	55			
Db		509	TTCCACAAGGCCATCA GAACAAGGTAGGTCTTTCTGCTATGGGGGCTGCAAGAC	56			
Oy		559	TGGAAGGCGGGGGCGACCCCTGTGA CGAGCA TTGCCA GTGTTCCCACTGTCAAGTTC	61			
Db		569	TGGAAGGCGGGGGCGACCCCTGTGA CGAGCA TTGCCA GTGTTCCCACTGTCAAGTTC	62			
Oy		619	CTGCTCCGCTCA AAGGAAAGACTTTGTGCA CAGTGTGCAAGAGACTCATCCACGTG	67			
Db		629	CTGCTCCGCTCA AAGGAAAGACTTTGTGCA CAGTGTGCAAGAGACTCATCCACGTG	68			
Oy		679	CTGGGCTCTCGGGAGCCCGTGGGAAAGAACCGGAAGCGAGCCCTGTGGCCCCCTCCGTC	72			
Db		689	CTGGGCTCTCGGGAGCCCGTGGGAAAGAACCGGAAGCGAGCCCTGTGGCCCCCTCCGTC	74			
Oy		739	CTGCTCTTGGGATACCTTAGCTGGCCCA CACCAGAGAGAGAGTCCAGTCTGA AAGTGC	79			
Db		749	CTGCTCTTGGGATACCTTAGCTGGCCCA CACCAGAGAGAGAGTCCAGTCTGA AAGTGC	80			
Oy		799	CAGAGCGCAGGAG	81			
Db		809	CAGAGCGCAGGAG	82			
<hr/>							
RESULT 11							
ID	AAA15007	standard; cDNA; 1563 BP.					
XX	AAA15007;						
XX	21-ANG-2000	(first entry)					
DE	cDNA encoding a human proliferation and apoptosis related protein.						
KW	Human: proliferative and apoptosis related protein; PROAP; psoriasis;						
KW	cell proliferative disorder; immunological disorder; hepatitis;						
KW	reproductive disorder; arteriosclerosis; dermatosis; melanoma; lymphoma;						
KW	cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia;						
KW	asthma; diabetes mellitus; osteoarthritis; endometritis;						

KW uterine fibroid; menstrual cycle; ss.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH CDS 215..1111
 FT /*tag= a
 FT /product= "proliferation and apoptosis related protein"
 XX
 XX WO20023589-A2.
 XX
 XX 27-APR-2000.
 PD
 XX
 XX 19-OCT-1999; 99WO-US024511.
 PE
 XX 20-OCT-1998; 98US-0172216P.
 PR 04-FEB-1999; 99US-0118559P.
 PR 11-FEB-1999; 99US-0172229P.
 PR 22-APR-1999; 99US-0154336P.
 XX
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Tang YT, Yue H, Hillman JL, Guegler KJ, Corley NC, Lal P;
 PI Azimzai Y, Baughn MR, Yang J, Shih LL;
 PI WPI: 2000-339688/29.
 DR P-PSDB; AAY84907.
 XX
 XX New human proliferation and apoptosis related protein polypeptides used
 PT for diagnosis, treatment and prevention of cell proliferative,
 PT immunological and reproductive disorders.
 XX
 XX
 PS Claim 9, Page 121; 128pp; English.
 XX
 CC The present sequence encodes a human proliferation and apoptosis related
 CC protein (PROAP). The polypeptides and polynucleotides can be used for the
 CC diagnosis, treatment and prevention of cell proliferative, immunological
 CC and reproductive disorders. Disorders associated with decreased
 CC expression or activity of include arteriosclerosis, cirrhosis, hepatitis,
 CC psoriasis, melanoma, lymphoma and cancers of the breast, brain and
 CC prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemia,
 CC asthma, diabetes mellitus, osteoarthritis, endometriosis, uterine
 CC fibroids and disruptions of the menstrual cycle. Antibodies against PROAP
 CC can be used in diagnosis of disorders characterized by PROAP e.g. in ELISA
 CC (enzyme linked immunosorbent assays) and the polynucleotides may be used
 CC to detect and quantify gene expression in biopsied tissues. These
 CC techniques can also be used to monitor regulation of PROAP levels during
 CC therapeutic intervention
 CC
 SQ Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;
 Query Match 59.6%; Score 742; DB 3; Length 1363;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 19 GGCAGGCTTGCTGCTATTCCTGCTGTCCTCCCGAGGCTGGGCGGTGAGAGCTCCAG 78
 DB 74 GGCAGGCTTGCTGCTATTCCTGCTGTCCTCCCGAGGCTGGGCGGTGAGAGCTCCAG 133
 QY 79 AAGGCGCAGTGGGATATTCGATGAGATGAGCATCAGCCCATTTCTGCTGCAAACTCG 138
 DB 134 AAGGCGCAGTGGGATATTCGATGAGATGAGCATCAGCCCATTTCTGCTGCAAACTCG 193
 QY 139 GTCAGAGCAGTGTTCCTTCATGAGGACTTAAGACAGTGCCTGCTGACCTGGA 198
 DB 194 GTCAGAGCAGTGTTCCTTCATGAGGACTTAAGACAGTGCCTGCTGACCTGGA 253
 QY 199 CCAAGAGCCGAGCCACTGGGAGCCGGGTATGCTCCCAAGAGAGCGGTGTGACCCCGC 258
 DB 254 CCAAGAGCCGAGCCACTGGGAGCCGGGTATGCTCCCAAGAGAGCGGTGTGACCCCGC 313
 QY 259 TCTCTGGGCAAGCCCTGCTCTGAGGCTGAGACCTGAGAGCCTGGAGCAAGTGGATGGG 318

DB 314 TCTCTGGGCAAGCCCTGCTCTAGAGCTTGACACCTTGACAGAGCTTGGACACAGTGGATGGG 373
 QY 319 CAGATCCTGGGCCAGCTGCGGCCCTTCAGACAGAGAGAGAGAGAGAGGCGCGGGGCC 378
 DB 374 CAGATCCTGGGCCAGCTGCGGCCCTTCAGACAGAGAGAGAGAGAGAGGCGCGGGGCC 433
 QY 379 ACCTTGTCCAGAGGGGCGCTGCTTCCCGGACATGGGCTCTGAGAGATTGCTTGGCTTCC 438
 DB 434 ACCTTGTCCAGAGGGGCGCTGCTTCCCGGACATGGGCTCTGAGAGATTGCTTGGCTTCC 493
 QY 439 TTCTATGACTGGCCGCTGACTGACTGAGTGCACCCGAGCTGCTGGCTGCGGGCTTC 498
 DB 494 TTCTATGACTGGCCGCTGACTGACTGAGTGCACCCGAGCTGCTGGCTGCGGGCTTC 553
 QY 499 TTCCACACAGGCCATCAGACCAAGTGAAGTGTCTTCTTGTCTATGGGGGCTTCAGAGC 558
 DB 554 TTCCACACAGGCCATCAGACCAAGTGAAGTGTCTTCTTGTCTATGGGGGCTTCAGAGC 613
 QY 559 TGGAAAGCGCGGGAGCAAGCCCTGAGCGAGCATGCCAAGTGTTCCTCCAGCTGCAGTTC 618
 DB 614 TGGAAAGCGCGGGAGCAAGCCCTGAGCGAGCATGCCAAGTGTTCCTCCAGCTGCAGTTC 673
 QY 619 CTGCTCCGCTCAAAAGAGAGACTTGTGCACAGTGTGACAGAGACTCATCCAGCTG 678
 DB 674 CTGCTCCGCTCAAAAGAGAGACTTGTGCACAGTGTGACAGAGACTCATCCAGCTG 733
 QY 679 CTGGGCTCTTGGGACCCGTTGGGAAAGAACCGAGAACCGAGCCCTGTGGCCCTCCGTC 738
 DB 734 CTGGGCTCTTGGGACCCGTTGGGAAAGAACCGAGAACCGAGCCCTGTGGCCCTCCGTC 793
 QY 739 CTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798
 DB 794 CTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853
 QY 799 CAGAGGCCAGAG 811
 DB 854 CAGAGGCCAGAG 866
 RESULT 12
 ID ADR88075 standard; cDNA; 1363 BP.
 XX ADR88075;
 AC ADR88075;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Human proliferation and apoptosis related protein (PROAP)-18 cDNA.
 XX
 KW PROAP; proliferation and apoptosis related protein;
 KW cell proliferative disorder; cancer; atherosclerosis;
 KW immunological disorder; AIDS; acquired immunodeficiency syndrome;
 KW allergy; reproductive disorder; infertility; gene therapy; cytostatic;
 KW antiarteriosclerotic; immunosuppressive; anti-HIV; anti-allergic;
 KW anti-infertility; gynaecological; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 215..1111
 FT /*tag= a
 FT /product= "Proliferation and apoptosis related protein
 FT (PROAP)-18"
 XX
 XX US2004203106-A1.
 PD 14-OCT-2004.
 XX
 XX 05-MAY-2004; 2004US-00839882.
 PF
 XX
 XX 19-JAN-1999; 99US-0172216P.
 PR 04-FEB-1999; 99US-0118559P.
 PR 11-FEB-1999; 99US-0172229P.

```

PR 22-APR-1999; 99US-0154336P.
PR 19-OCT-1999; 99MO-US024511.
PR 11-APR-2001; 2001US-00807452.
XX
XX (INCYTE) INCYTE CORP.
XX
XX Tang YF, Yue H, Hillman JL, Guegler KJ, Corley NC, Lal P;
XX P1 Azimzal Y, Baughn MR, Yang J, Shin LI;
XX P2 WPI: 2004-728011/71.
XX P-PSDB; ADT86056.
XX
XX New human proliferation and apoptosis related proteins and
XX PT polynucleotides for diagnosing, preventing or treating disorders
XX PT associated with aberrant protein expression, e.g. cancer, AIDS,
XX PT atherosclerosis or infertility.
XX
XX PS Claim 5; SEQ ID NO 37; 85pp; English.
XX
XX The present invention relates to the human proliferation and apoptosis
XX CC related protein (PROAP) and its encoding nucleic acid. The invention is
XX CC useful for diagnosing, preventing or treating disorders associated with
XX CC altered expression or activity of human PROAP, such as cell proliferative
XX CC (e.g. cancer or atherosclerosis), immunological (e.g. acquired
XX CC immunodeficiency syndrome (AIDS) or allergies) or reproductive (e.g.
XX CC infertility) disorders. The invention is also be used in screening for
XX CC drugs that may be used for treating or preventing the disorders mentioned
XX CC above and in gene therapy. The present sequence is the human PROAP-18
XX CC protein encoding cDNA.
XX
XX Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;
SQ
Query Match 59.6%; Score 742; DB 13; Length 1363;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 19 GGGAGGCTGTGCTTATCCCTGCTGCTGCCAGAGGTGGGCGGGGGGTGAGAGCTCCAG 78
DB 74 GGGAGGCTGTGCTTATCCCTGCTGCTGCCAGAGGTGGGCGGGGGGTGAGAGCTCCAG 133
QY 79 AAGGGCCAGCTGGGCGCATATTTGAGATTGGCCATACAGCCCATTTCTGCTGCAAACTTG 138
DB 134 AAGGGCCAGCTGGGCGCATATTTGAGATTGGCCATACAGCCCATTTCTGCTGCAAACTTG 193
QY 139 GTTAGAGCCAGTGTTCCTTCATAGGACCTTAAGACAGTGCCTGCAACCTGGA 198
DB 194 GTTAGAGCCAGTGTTCCTTCATAGGACCTTAAGACAGTGCCTGCAACCTGGA 253
QY 199 CCACAGCCGAGCCAGCTGGGCGCGGTATGTGCTCCACAGCAGAGCCGTGTGAGCCCGC 258
DB 254 CCACAGCCGAGCCAGCTGGGCGCGGTATGTGCTCCACAGCAGAGCCGTGTGAGCCCGC 313
QY 259 TCTCTGGGAGCCCTGTCTTAGGCTTGACACCTTCAGAGCTGGGACCATGTGATGG 318
DB 314 TCTCTGGGAGCCCTGTCTTAGGCTTGACACCTTCAGAGCTGGGACCATGTGATGG 373
QY 319 CAGATCTGTGGGCGCAGCTGGGCGCGGTATGTGCTCCACAGCAGAGCCGTGTGAGCCCGC 378
DB 374 CAGATCTGTGGGCGCAGCTGGGCGCGGTATGTGCTCCACAGCAGAGCCGTGTGAGCCCGC 433
QY 379 ACCCTGTCCAGGGGCGCTGCTTCCCGGCGCATGGGCTTGAGAGGTTGCGTGGCCCTCC 438
DB 434 ACCCTGTCCAGGGGCGCTGCTTCCCGGCGCATGGGCTTGAGAGGTTGCGTGGCCCTCC 493
QY 439 TTTCTATGATGGGCGCGCTGATGCTGAGAGTGCACCCGAGCTGTGGCTGCTGCCGGCTTC 498
DB 494 TTTCTATGATGGGCGCGCTGATGCTGAGAGTGCACCCGAGCTGTGGCTGCTGCCGGCTTC 553
QY 499 TTTCACACAGGCGCATCAGAGCAAGGTAGGCTTTCTTCTGCTATGGGGGCTTGCAAGC 558
DB 554 TTTCACACAGGCGCATCAGAGCAAGGTAGGCTTTCTTCTGCTATGGGGGCTTGCAAGC 613
QY 559 TGGAAAGCGGGGAGCAGACCTCTGAGACGAGCATGCAAGTGTTCCTCCAGCTGTCACTTC 618

```

```

DB 614 TGGAAAGCGGGGAGCAGACCTCTGAGCGAGCATGCAAGTGTTCCTCCAGCTGTCACTTC 673
QY 619 CTGCTCCGGTCAAAAAGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 678
DB 674 CTGCTCCGGTCAAAAAGAGACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTG 733
QY 679 CTGGGCTCTCGGGACCCGCTGGGAGAAACCCGAAACCGACGCCCTGTGGCCCTCCGTC 738
DB 734 CTGGGCTCTCGGGACCCGCTGGGAGAAACCCGAAACCGACGCCCTGTGGCCCTCCGTC 793
QY 739 CTGCTCTGTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCTGAAAGTGGC 798
DB 794 CTGCTCTGTGGGTAACCTGAGCTGCCACACCCAGAGAGAGTCTGAAAGTGGC 853
QY 799 CAGAGCCAGAGAG 811
DB 854 CAGAGCCAGAGAG 866

```

```

RESULT 13
AD025445
ID AD025445 standard; DNA; 858 BP.
XX
XX AD025445;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 8265.
DE
XX
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW
XX
XX ds.
OS
XX
XX Homo sapiens.
PN
XX
XX MO2004048938-A2.
PD
XX
XX 10-JUN-2004.
PE
XX
XX 26-NOV-2003; 2003MO-US038193.
PR
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
PA
XX
XX Aziz N, Ginsburg WM, Zlotnik A;
PI
XX
XX WPI: 2004-441208/41.
DR
XX
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX Example 2; SEQ ID NO 8265; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX CC which comprises obtaining a first soft tissue sample from an individual
XX CC and a normal soft tissue sample from the same or different individual,
XX CC determining the expression of a gene in both samples and comparing the
XX CC expression of the gene in both soft tissue samples, where a higher level
XX CC of protein expression in the first soft tissue sample indicates the
XX CC presence of soft tissue sarcoma. The method of the invention has
XX CC cytostatic applications and may be useful for detecting soft tissue
XX CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX CC acid sequences may be useful in diagnostic and screening applications.
XX CC The current sequence is that of a human soft tissue sarcoma-upregulated
XX CC DNA of the invention. The current sequence is not shown within the
XX CC specification per se but was submitted in CD format by the inventor.
SQ
Sequence 858 BP; 169 A; 267 C; 269 G; 153 T; 0 U; 0 Other;
Query Match 51.2%; Score 638; DB 12; Length 858;

```


ORIGIN

Query Match 57.4%; Score 715; DB 5; Length 884;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TTCTGAGATTGGCCATCAGCCCATTTCTGCTGCAAACTGGTCAAGCAAGTGTTCCTCC
 Db 1 TTCTGAGATTGGCCATCAGCCCATTTCTGCTGCAAACTGGTCAAGCAAGTGTTCCTCC
 QY 157 TCCTAGGAGCCTTAAGAAGAGTCCAGTGTGCTGCAAGCCTGGAACAAGCCAGGCACTG
 Db 61 TCCTAGGAGCCTTAAGAAGAGTCCAGTGTGCTGCAAGCCTGGAACAAGCCAGGCACTG
 QY 217 GCACCCGCTGATGCTTCCCAAGCAGAGCCTGTGAGACCCGCTCTCTGAGGAGCCCTGTC
 Db 121 GCACCCGCTGATGCTTCCCAAGCAGAGCCTGTGAGACCCGCTCTCTGAGGAGCCCTGTC
 QY 277 CTAGGCTGAGACCTGCAAGCCTGGAACAAGTGTGAGATCCCTGGGCGCAGCTG 336
 Db 181 CTAGGCTGAGACCTGCAAGCCTGGAACAAGTGTGAGATCCCTGGGCGCAGCTG 240
 QY 337 CGGCCCCCTGACAGAGGAGAAAGAGAGAGGCGCGGCGCACTTGTCCAGGGGCGCT 396
 Db 241 CGGCCCCCTGACAGAGGAGAAAGAGAGAGGCGCGGCGCACTTGTCCAGGGGCGCT 300
 QY 397 GCCTTCCCGGCAATGGGCTCTGAGAGAGTGTGCTGGCCCTCTTATGACTGGCCGCTG 456
 Db 301 GCCTTCCCGGCAATGGGCTCTGAGAGAGTGTGCTGGCCCTCTTATGACTGGCCGCTG 360
 QY 457 ACTGCTGAGTGTCCACCCGAGCTGTGAGCTGTCCGAGCTTCTCCACAGAGCCATCAG 516
 Db 361 ACTGCTGAGTGTCCACCCGAGCTGTGAGCTGTCCGAGCTTCTCCACAGAGCCATCAG 420
 QY 517 GACAAGGTGAGGTCTTCTTCTGCTATGAGGAGGCTTCAAGCTGGAAGCGCGGAGACAG 576
 Db 421 GACAAGGTGAGGTCTTCTTCTGCTATGAGGAGGCTTCAAGCTGGAAGCGCGGAGACAG 480
 QY 577 CCCTGAGCAGAGCATCCCAAGTGTGCCCAAGCTGTCACTTCCTGCTCCGCTCAAAAGGA 636
 Db 481 CCCTGAGCAGAGCATCCCAAGTGTGCCCAAGTGTCACTTCCTGCTCCGCTCAAAAGGA 540
 QY 637 AGAGACTTTGTCCACAGTGTGCAAGAGACTCACTCCAGCTGCTGGGCTCTCCAGAGCCG 696
 Db 541 AGAGACTTTGTCCACAGTGTGCAAGAGACTCACTCCAGCTGCTGGGCTCTCCAGAGCCG 600
 QY 697 TGGGAAGAACCGGAAGCAGAGCCCTGTGGCCCTCCGCTCCGCTCTGGGTAACCTT 756
 Db 601 TGGGAAGAACCGGAAGCAGAGCCCTGTGGCCCTCCGCTCCGCTCTGGGTAACCTT 660
 QY 757 GAGCTCCCAACACCCGAGAGAGAGTTCAGTCTGAAAGTCCCAAGAGCCAGAGAG 811
 Db 661 GAGCTCCCAACACCCGAGAGAGAGTTCAGTCTGAAAGTCCCAAGAGCCAGAGAG 715

RESULT 2

BO682827 924 bp mRNA linear EST 15-JUL-2002
 LOCUS BO682827
 DEFINITION AGENCOURT_8507903 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6294748
 5', mRNA sequence.

ACCESSION BO682827
 VERSION BO682827.1 GI:21795506
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 924)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9apbs@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNC2499 row: 0 column: 05
 High quality sequence stop: 673.

FEATURES

source

1..924

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6294748"

/tissue_type="melanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 57.4%; Score 715; DB 5; Length 924;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TTCTGAGATTGGCCATCAGCCCATTTCTGCTGCAAACTGGTCAAGCAAGTGTTCCTCC
 Db 1 TTCTGAGATTGGCCATCAGCCCATTTCTGCTGCAAACTGGTCAAGCAAGTGTTCCTCC
 QY 157 TCCTAGGAGCCTTAAGAAGAGTCCAGTGTGCTGCAAGCCTGGAACAAGCCAGGCACTG 216
 Db 61 TCCTAGGAGCCTTAAGAAGAGTCCAGTGTGCTGCAAGCCTGGAACAAGCCAGGCACTG 120
 QY 217 GCACCCGCTGATGCTTCCCAAGCAGAGCCTGTGAGACCCGCTCTTGGGAGCCCTGTC 276
 Db 121 GCACCCGCTGATGCTTCCCAAGCAGAGCCTGTGAGACCCGCTCTTGGGAGCCCTGTC 180
 QY 277 CTAGGCTGAGACCTGCAAGCCTGGAACAAGTGTGAGATCCCTGGGCGCAGCTG 336
 Db 181 CTAGGCTGAGACCTGCAAGCCTGGAACAAGTGTGAGATCCCTGGGCGCAGCTG 240
 QY 337 CGGCCCCCTGACAGAGGAGAAAGAGAGAGGCGCGGCGCACTTGTCCAGGGGCGCT 396
 Db 241 CGGCCCCCTGACAGAGGAGAAAGAGAGAGGCGCGGCGCACTTGTCCAGGGGCGCT 300
 QY 397 GCCTTCCCGGCAATGGGCTCTGAGAGAGTGTGCTGGCCCTCTTATGACTGGCCGCTG 456
 Db 301 GCCTTCCCGGCAATGGGCTCTGAGAGAGTGTGCTGGCCCTCTTATGACTGGCCGCTG 360
 QY 457 ACTGCTGAGTGTCCACAGCTGTGCTGTGCTGCGGCTTCTTCCACAGAGCCATCAG 516
 Db 361 ACTGCTGAGTGTCCACAGCTGTGCTGTGCTGCGGCTTCTTCCACAGAGCCATCAG 420
 QY 517 GACAAGGTGAGGTCTTCTTCTGCTATGAGGAGGCTGCAAGCTGGAACCGCGGAGACAG 576
 Db 421 GACAAGGTGAGGTCTTCTTCTGCTATGAGGAGGCTGCAAGCTGGAACCGCGGAGACAG 480
 QY 577 CCTGAGCAGAGCATCCCAAGTGTTCCTCCAGCTGTCACTTCCTGCTCCGCTCAAAAGGA 636
 Db 481 CCTGAGCAGAGCATCCCAAGTGTTCCTCCAGCTGTCACTTCCTGCTCCGCTCAAAAGGA 540
 QY 637 AGAGACTTTGTCCACAGTGTGCAAGAGACTCACTCCAGCTGCTGGGCTCTCCAGAGCCG 696
 Db 541 AGAGACTTTGTCCACAGTGTGCAAGAGACTCACTCCAGCTGCTGGGCTCTCCAGAGCCG 600

QY 697 TGGAGAGACCGGAGAGACGACCCCTGCGCCCTCCCTGCTGCGGACCT 756
DB 601 TGGAGAGACCGGAGAGACGACCCCTGCGCCCTCCCTGCTGCGGACCT 660
QY 757 GAGCTGCCACACCGGAGAGAGGTTCAGTCTGAAGTGCAGAGCCAGAG 811
DB 661 GAGCTGCCACACCGGAGAGAGGTTCAGTCTGAAGTGCAGAGCCAGAG 715

RESULT 3
LOCUS B0892691
DEFINITION AGENCOURT 8095843 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6087832
5', mRNA sequence.
ACCESSION B0892691
VERSION B0892691.1 GI:22284705
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 929)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LNCM2325 row: a column: 17
High quality sequence stop: 628.
Location/Qualifiers

FEATURES
source

1. 929
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6087832"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_112"
/note="Organ: skin; Vector: pOB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."

ORIGIN

Query Match 56.3%; Score 701; DB 5; Length 929;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 AGCTCCAGAGAGGCGAGCTGGGCAATTCAGATTGGCCATCGACCCCATTTCTGCTG 130
DB 1 AGCTCCAGAGAGGCGAGCTGGGCAATTCAGATTGGCCATCGACCCCATTTCTGCTG 60
QY 131 CAAACCTGTGAGAGCGAGTGTCCCTCCATGAGGACCTAAAGACAGTGCCTGCTGC 190
DB 61 CAAACCTGTGAGAGCGAGTGTCCCTCCATGAGGACCTAAAGACAGTGCCTGCTGC 120
QY 191 ACCGTGAGACACAGCCGAGCCACTGGGCAAGCGGTGATGTCCTCCAGAGAGGCGCTGTG 250
DB 121 ACCGTGAGACACAGCCGAGCCACTGGGCAAGCGGTGATGTCCTCCAGAGAGGCGCTGTG 180
QY 251 GACCCCGCTCTCTGGGAGCCCTGTCTTAAGGCTTGAGACCTGGACAGGCTGGAGCACAG 310

DB 181 GACCCCGCTCTCTGGGAGCCCTGTCTTAAGGCTTGAGACCTGGACAGGCTGGAGCACAG 240
QY 311 TGGATGGGACAGATCTGTGGGCGAGCTGGGCGCCCTGACAGAGAGAGAGAGAGGCG 370
DB 241 TGGATGGGACAGATCTGTGGGCGAGCTGGGCGCCCTGACAGAGAGAGAGAGAGGCG 300
QY 371 CCGGAGGCGACCTGTTCAGAGGGGCGCTGCTTCCCGGCATGGGCTTGAGAGATTGCGTC 430
DB 301 CCGGAGGCGACCTGTTCAGAGGGGCGCTGCTTCCCGGCATGGGCTTGAGAGATTGCGTC 360
QY 431 TGGGCTCTCTTATAGACTGGCGCGCTGACTGTGAGTGGCCACCCGACCTGTGCTCTG 490
DB 361 TGGGCTCTCTTATAGACTGGCGCGCTGACTGTGAGTGGCCACCCGACCTGTGCTCTG 420
QY 491 CCGGCTTCTTCAACACAGGCGCATGAGACCAAGTGAAGTCTTCTGCTATGAGGAGCC 550
DB 421 CCGGCTTCTTCAACACAGGCGCATGAGACCAAGTGAAGTCTTCTGCTATGAGGAGCC 480
QY 551 TGCAGAGCTGGAGAGCGGCGGAGCGACCTTGAGACGAGCATGCGAAGTGTTCGCCAGCT 610
DB 481 TGCAGAGCTGGAGAGCGGCGGAGCGACCTTGAGACGAGCATGCGAAGTGTTCGCCAGCT 540
QY 611 GTGAGTCTGCTGCTCGGTCGAAAGAGAGACTTGTCCACAGTGTGACAGAGACTACT 670
DB 541 GTGAGTCTGCTGCTCGGTCGAAAGAGAGACTTGTCCACAGTGTGACAGAGACTACT 600
QY 671 CCGAGCTGCTGGGCTCTGCGGAGACCCGTGGAGAGAACCGAAGACGACCCCTGTGCGCC 730
DB 601 CCGAGCTGCTGGGCTCTGCGGAGACCCGTGGAGAGAACCGAAGACGACCCCTGTGCGCC 660
QY 731 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
DB 661 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 701

RESULT 4

B0682897

LOCUS

DEFINITION

AGENCOURT 8210542 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6259145

5', mRNA sequence.

ACCESSION

B0682897

VERSION

B0682897.1 GI:21795576

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens (human)

Eukaryota;

Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

Mammalia;

Eutheria;

Euarchontoglires;

Primates;

Catarrhini;

Hominae;

Homo.

1 (bases 1 to 982)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

http://image.llnl.gov

Plate: LNCM2416 row: c column: 18

High quality sequence stop: 623.

Location/Qualifiers

1. 982

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6259145"

/tissue_type="melanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_1lb="NIH_MGC_112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 55.7%; Score 694; DB 5; Length 982;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 97 TTCTGAGATTGGCCATTCAGCCCCATTTCTGCTCAAACTGTGACAGGCAGTGTTC 156
DB 1 TTCTGAGATTGGCCATTCAGCCCCATTTCTGCTCAAACTGTGACAGGCAGTGTTC 60
QY 157 TCCATGGGACCTTAAGACAGTGGCCAGTGCCTGACCGTGGACACACAGCCGACCTG 216
DB 61 TCCATGGGACCTTAAGACAGTGGCCAGTGCCTGACCGTGGACACACAGCCGACCTG 120
QY 217 GCACCCGCTGATGTTCCACGACGAGCGCTGTGACCCCGCTCTCTGGACAGCCCTGTC 276
DB 121 GCACCCGCTGATGTTCCACGACGAGCGCTGTGACCCCGCTCTCTGGACAGCCCTGTC 180
QY 277 CTAGGCTTGAACACTTGCAGAGCCTGGGACACAGTGGATGGAGATCTTGGGCGACGTG 336
DB 181 CTAGGCTTGAACACTTGCAGAGCCTGGGACACAGTGGATGGAGATCTTGGGCGACGTG 240
QY 337 CGGCGCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
DB 241 CGGCGCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 397 GCGCTTCCCGGCAATGGGCTCTGAGAGAGTTCCTGCTGCTCTCTATGACTGGCCGCTG 456
DB 301 GCGCTTCCCGGCAATGGGCTCTGAGAGAGTTCCTGCTGCTCTCTATGACTGGCCGCTG 360
QY 457 ACTGCTGAGGTGCACCCGAGCTGTGCTGCTGCGGCTTCTTCCACAGAGCCCATAG 516
DB 361 ACTGCTGAGGTGCACCCGAGCTGTGCTGCTGCGGCTTCTTCCACAGAGCCCATAG 420
QY 517 GACAGGTTGAGTGTCTTCTGCTATGGGGCTGTGACAGAGTGGAAAGCGCGGAGCGAC 576
DB 421 GACAGGTTGAGTGTCTTCTGCTATGGGGCTGTGACAGAGTGGAAAGCGCGGAGCGAC 480
QY 577 CCCTGAGCGAGGATGCCAAGTGTTCCTCCAGCTGTCAAGTTCCTGCTCCGGTCAAAA 636
DB 481 CCCTGAGCGAGGATGCCAAGTGTTCCTCCAGCTGTCAAGTTCCTGCTCCGGTCAAAA 540
QY 637 AGAGACTTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTCTGGGACCG 696
DB 541 AGAGACTTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTCTGGGACCG 600
QY 697 TGGAGAGAACCGGAGAGACGACCCCTGTGGCCCTCCCTGCTCTGGGTAACCT 756
DB 601 TGGAGAGAACCGGAGAGACGACCCCTGTGGCCCTCCCTGCTCTGGGTAACCT 660
QY 757 GAGCTGCTCCACACCCAGAGAGAGAGTCCAGTCTG 790
DB 661 GAGCTGCTCCACACCCAGAGAGAGAGTCCAGTCTG 694

```

RESULT 5
BU180020
LOCUS BU180020 945 bp mRNA linear EST 04-SEP-2002
DEFINITION AGENCOURT_8106750 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6253787
ACCESSION BU180020
VERSION BU180020.1 GI:22694004
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@dbi-remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1CM2402 row: d column: 12
High quality sequence start: 13
High quality sequence stop: 667.
Location/Qualifiers
1. 945

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6253787"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 53.9%; Score 672; DB 5; Length 945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 96 ATTCTGAGTATGGCCATTCAGCCCCATTTCTGCTCAAACTGTGACAGGCAGTGTTC 155
DB 26 ATTCTGAGTATGGCCATTCAGCCCCATTTCTGCTCAAACTGTGACAGGCAGTGTTC 85
QY 156 CTCCATGAGACCTTAAGACAGTGGCCAGTGCCTGACCGTGGACCAAGCCGAGCACTG 215
DB 86 CTCCATGAGACCTTAAGACAGTGGCCAGTGCCTGACCGTGGACCAAGCCGAGCACTG 145
QY 216 GGCAGCCGCTGATGTTCCACGACGAGCGCTGTGACCCCGCTCTTGGGACGCTGT 275
DB 146 GGCAGCCGCTGATGTTCCACGACGAGCGCTGTGACCCCGCTCTTGGGACGCTGT 205
QY 276 CTAAGGCTTGAACACTTGCAGAGCCTGGGACACAGTGGATGGGACAGATCTTGGGCA 335
DB 206 CTAAGGCTTGAACACTTGCAGAGCCTGGGACACAGTGGATGGGACAGATCTTGGGCA 265
QY 336 GCGGCCCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 395
DB 266 GCGGCCCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 325
QY 396 TGCCTTCCCGGCAATGGGCTCTGAGAGATTCGCTGTGGCTCTCTTCTATGACTGGCCGT 455
DB 326 TGCCTTCCCGGCAATGGGCTCTGAGAGATTCGCTGTGGCTCTCTTCTATGACTGGCCGT 385
QY 456 GACTGCTGAGGTGCCACCGAGCTGTGCTGTGCGGCTTCTTCCACACAGGCCATCA 515
DB 386 GACTGCTGAGGTGCCACCGAGCTGTGCTGTGCGGCTTCTTCCACACAGGCCATCA 445
QY 516 GGAAGAAGTGAAGTGTCTTCTGCTATGGGGCTTGCACAGCTGGAAGCGCGGAGCGA 575
DB 446 GGAAGAAGTGAAGTGTCTTCTGCTATGGGGCTTGCACAGCTGGAAGCGCGGAGCGA 505

```


OY	576	CCCCGAGACGGAGCATGCGCAAGTGGTTCCCGACGCTGAGTTCGCGTCCGGTCAAAAAG	635
Dp	506	CCCCGAGACGGAGCATGCGCAAGTGGTTCCCGACGCTGAGTTCGCGTCCGGTCAAAAAG	565
OY	636	AAGACACTTTGTCCACAGTGTGCAGAGAGACTCAGTCCAGCTGTGAGGCTCCTCGGAGACC	695
Dp	566	AAGAGACTTTGTCCACAGTGTGCAGAGAGACTCAGTCCAGCTGTGAGGCTCCTCGGAGACC	625
OY	696	GTGGGAATAACCCGGAAGACGAGCCCCCTGTGGCCCCCTCCGTCCTCTGTGGGTACCC	755
Dp	626	GTGGGAATAACCCGGAAGACGAGCCCCCTGTGGCCCCCTCCGTCCTCTGTGGGTACCC	685
OY	756	TGAGCTGCCAC 767	
Dp	686	TGAGCTGCCAC 697	
RESULT 6			
BOG82378			
LOCUS		912 bp	mRNA linear EST 15-JUL-2002
DEFINITION	AGNCOURT 818584 NIH_MGC_112 Homo sapiens CDNA clone IMAGE:6263255		
ACCESSION	BOG82378		
VERSION	BOG82378.1	GI:21795057	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo		
REFERENCE	1 (bases 1 to 912)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LNCM2426 row: n column: 24 High quality sequence stop: 609. Location/Qualifiers		
FEATURES			
source			1..912

ORIGIN

Query Match	52.9%	Score 659	DB 5	Length 912
Best Local Similarity	99.9%	Pred. No. 0		
Matches	709	Conservative	0	Mismatches 1; Indels 0; Gaps 0
Qy	97	TTCTGAGCATTTGGCCATCAGCCCCATTTTCTGCTGCAGAAACCTGTGAGAGCCAGTGTCC	156	
Db	1	TTCTGAGATTTGGCCATTCAGCCCCATTTTCTGCTGCAGAAACCTGTGAGAGCCAGTGTCC	60	

[illegible]

RESULT	7
LOCUS	BUI188703
DEFINITION	BUI188703 958 bp mRNA linear EST 04-SEP-2002 ACENCCOURT 7662186 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6106302
ACCESION	BUI188703
VERSION	5, mRNA sequence.
KEYWORDS	BUI188703.1 GI:22702687
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 958) NIH-MGC http://mgc.nci.nih.gov/ , National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

cDNA library Preparation: Rubin Laboratory
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2347 row: c column: 07
 High quality sequence start: 12

FEATURES
source High quality sequence stop: 611.
Location/Qualifiers
1..958

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6106302"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_112"
/note="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 51.4%; Score 641; DB 5; Length 958;
Best Local Similarity 100.0%; Pred. No. 1.1e-307; Indels 0; Gaps 0;
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 GGCAGGCTTGTGCTATTCCTGCTGTCCTCCAGGGTGGGCGCGGGGTGAGAGTCCAG 78
64 GGCAGGCTTGTGCTATTCCTGCTGTCCTCCAGGGTGGGCGCGGGGTGAGAGTCCAG 123
79 AAGGCGCAGTGTGCTATTCCTGCTGTCCTCCAGGGTGGGCGCGGGGTGAGAGTCCAG 138
124 AAGGCGCAGTGTGCTATTCCTGCTGTCCTCCAGGGTGGGCGCGGGGTGAGAGTCCAG 183
139 GTGAGAGCAGTGTGCTATTCCTGCTGTCCTCCAGGGTGGGCGCGGGGTGAGAGTCCAG 198
184 GTGAGAGCAGTGTGCTATTCCTGCTGTCCTCCAGGGTGGGCGCGGGGTGAGAGTCCAG 243
199 CCAGAGCCGAGCAGTGTGCTATTCCTGCTGTCCTCCAGGGTGGGCGCGGGGTGAGAGTCCAG 258
244 CCAGAGCCGAGCAGTGTGCTATTCCTGCTGTCCTCCAGGGTGGGCGCGGGGTGAGAGTCCAG 303
259 TCTCTGGGCGAGCCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 318
304 TCTCTGGGCGAGCCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 363
319 CAGATCCTGGGCGAGCCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 378
364 CAGATCCTGGGCGAGCCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 423
379 ACCCTGTCCAGAGGCGCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 438
424 ACCCTGTCCAGAGGCGCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 483
439 TTCTATGAGCTGGGCGCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 498
484 TTCTATGAGCTGGGCGCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 543
499 TTCTATGAGCTGGGCGCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 558
544 TTCTATGAGCTGGGCGCTGCTGCTGAGGCTGAGCAGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 603
559 TGGAGAGCGGGGAGAGCAGCCTGAGAGCAGAGTGGATGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 618
604 TGGAGAGCGGGGAGAGCAGCCTGAGAGCAGAGTGGATGCTGAGAGCCTGAGAGCCTGAGAGTCCAG 663
619 CTGCTCCGGGTCAAAAGAGAGCTTTTCCAGAGTGGCA 659
664 CTGCTCCGGGTCAAAAGAGAGACTTTTCCAGAGTGGCA 704

RESULT 8
CD673774 621 bp mRNA linear EST 24-JUN-2003
LOCUS CD673774
DEFINITION f804c01.y2 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone

ACCESSION f804c01.5', mRNA sequence.

VERSION CD673774.1 GI:32175505

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 621)

AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,

Boulford,G., Smith,D., and Peterson,K.

Expressed sequence tag analysis of adult human lens for the NetBank

Project: over 2000 non-redundant transcripts, novel genes and

splice variants

Mol. Vis. 8 (4), 171-184 (2002)

12107413

COMMENT Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 04 row: C column: 01

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1..621

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="f804c01"

/tissue_type="Lens"

/dev_stage="Adult"

/lab_host="EMDH10B"

/note="Organ: Eye; Vector: pCMVSPORT6; A human lens

library (by) was normalized by self-subtraction. One

portion of double stranded plasmid DNA representing the

library was linearized by NotI. This NotI digested library

was used as a template for biotinylated RNA synthesis

using SP6 RNA polymerase. Another portion of the double

stranded plasmid library was converted to single-stranded

circles in vitro using Gene II and Exonuclease III (Life

Technologies). Single-stranded DNA (1 mg) was hybridized

(Cot 500) with 41 mg of Bio-RNA and vector blocking

oligonucleotides. The hybridized Bio-RNA/ss-circles were

removed by streptavidin:phenol extraction. EST analysis

was performed on the library at the NIH Intramural

ORIGIN

Query Match 49.8%; Score 621; DB 6; Length 621;
Best Local Similarity 100.0%; Pred. No. 1e-297;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

179 CCAAGTCTGTGACCGGTGAGACCAAGCGGAGCACTGGGCGAGCCGGTATGCTCCACGC 238
1 CCAAGTCTGTGACCGGTGAGACCAAGCGGAGCACTGGGCGAGCCGGTATGCTCCACGC 60
239 AGAAGCGCTGTGAGACCCGCTCTCTGAGCAGCCCTGTCTAGAGCCTGAGACCTGAGAG 298
61 AGAAGCGCTGTGAGACCCGCTCTCTGAGCAGCCGCTGTCTAGAGCCTGAGACCTGAGAG 120
229 CTTGGGACCAAGTGTGATGGAGGAGATCTCTGGGCGAGCTGGCCCTCTGACAGAGAG 358
121 CTTGGGACCAAGTGTGATGGAGGAGATCTCTGGGCGAGCTGGCCCTCTGACAGAGAG 180
359 AGAAGAGAGGCGCGGGGCACTTGTTCAGAGGGGCGTCCCTTCCGGGAGATGGGCTCTG 418
181 AGAAGAGAGGCGCGGGGCACTTGTTCAGAGGGGCGTCCCTTCCGGGAGATGGGCTCTG 240
419 AGAAGTTCGCTGTGCGCTCTTCTATGACGTGGCCGCTGACTGTGAGTGCACCCGAGC 478

```

Db      241 AGGAGTTCGCTGCGCTCTCTTCTATGAGCCGCTGAGCTGAGTGCACCCGAGC
Oy      479 TGTGGCTGCTGCGCGCTTCTTCCACAGAGCCATCAGACAGAGTGAAGTCTTCTTCT
Db      301 TGCTGGCTGCTGCGCGCTTCTTCCACAGAGCCATCAGACAGAGTGAAGTCTTCTTCT
Oy      539 GCTATGAGGGGCTGAGAGCTGGAAGCGCGGGAGAGACCCCTTGACGGAGCATGCCAAGT
Db      361 GCTATGAGGGGCTGAGAGCTGGAAGCGCGGGAGAGACCCCTTGACGGAGCATGCCAAGT
Oy      599 GATTCCCGAGCTGCTGAGTTCCTGCTCCGGTCAAAAGAGAGACTTTGTCACAGTGGC
Db      421 GATTCCCGAGCTGCTGAGTTCCTGCTCCGGTCAAAAGAGAGACTTTGTCACAGTGGC
Oy      659 AGGAGACTCACTCCGAGCTGCTGAGGCTCTGAGGACCCGTGGAGAAAGACCGAAGACGAG
Db      481 AGGAGACTCACTCCGAGCTGCTGAGGCTCTGAGGACCCGTGGAGAAAGACCGAAGACGAG
Oy      719 CCCCCTGAGGCCCCCTCCGCTCTGCTGCTGAGTACCTGAGCTGCCACACCCAGAGAG
Db      541 CCCCCTGAGGCCCCCTCCGCTCTGCTGCTGAGTACCTGAGCTGCCACACCCAGAGAG
Oy      779 AGGTCCAGTCTGAAAGTGCCC 799
Db      601 AGGTCCAGTCTGAAAGTGCCC 621

```

RESULT 9
Bg770578 824 bp mRNA linear EST 15-MAY-2001
LOCUS 602734106F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4859641 5',
DEFINITION mRNA sequence.
ACCESSION Bg770578
VERSION Bg770578.1 GI:14081231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 824)
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLCM1715 row: k column: 02
High quality sequence stop: 799.

FEATURES
Source
Location/Qualifiers
1..824
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4859641"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_49"
/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC

ORIGIN Library: |"
Query Match 49.2%; Score 613; DB 2; Length 824;
Best Local Similarity 100.0%; Pred. 9.9e-294;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy      19 GGCAGGCTGTGCTATTCCTGCTGCTCCAGAGGTGGGCCCCGGGGTCAAGAGCTCCAG
Db      31 GGCAGGCTGTGCTATTCCTGCTGCTCCAGAGGTGGGCCCCGGGGTCAAGAGCTCCAG
Oy      79 AAGGCCAGCTGGGCAATTTCTGAGATTGGCCATACACCCCATTTTGTCTGCAAACTG
Db      91 AAGGCCAGCTGGGCAATTTCTGAGATTGGCCATACACCCCATTTTGTCTGCAAACTG
Oy      139 GTCAGAGCCAGTGTTCCTCCATGGAGCTTAAGACAGTGCAGAGTCCCTGACCCGTGA
Db      151 GTCAGAGCCAGTGTTCCTCCATGGAGCTTAAGACAGTGCAGAGTCCCTGACCCGTGA
Oy      199 CCACAGCCGAGCCACTGAGGAGCCGATGATGTCACAGAGAGCGCTGTGACCCCGC
Db      211 CCACAGCCGAGCCACTGAGGAGCCGATGATGTCACAGAGAGCGCTGTGACCCCGC
Oy      259 TCTCTGGGCAAGCCCTGCTTCTAGGCTTGAGACCTGACAGAGCTGGAGACAGTGAATGG
Db      271 TCTCTGGGCAAGCCCTGCTTCTAGGCTTGAGACCTGACAGAGCTGGAGACAGTGAATGG
Oy      319 CAGATCCTGGGCAAGCTGAGGAGCCCTGACAGAGAGAGAGAGAGAGGCGCCGGGAGC
Db      331 CAGATCCTGGGCAAGCTGAGGAGCCCTGACAGAGAGAGAGAGAGAGGCGCCGGGAGC
Oy      379 ACCTTGTCCAGAGGAGGCTGCTTCCCGGAGATGGACTTGAAGAGTTCGCTGGCTCC
Db      391 ACCTTGTCCAGAGGAGGCTGCTTCCCGGAGATGGACTTGAAGAGTTCGCTGGCTCC
Oy      439 TTCTATATCTGGCGCTGACTGACTGAGTGTCCACCCGAGCTGCTGCTGCGGCTTC
Db      451 TTCTATATCTGGCGCTGACTGACTGAGTGTCCACCCGAGCTGCTGCTGCGGCTTC
Oy      499 TTCACACAGAGCCATCAGACAGAGTGAAGTCTTCTGCTATGAGGAGCTTCACAGC
Db      511 TTCACACAGAGCCATCAGACAGAGTGAAGTGTCTTCTGCTATGAGGAGCTTCACAGC
Oy      559 TGAAGGCGGGAGAGAGACCCCTGAGCGAGCATGCCAAGTGTTCCTCCACCTGCTC
Db      571 TGAAGGCGGGAGAGAGACCCCTGAGCGAGCATGCCAAGTGTTCCTCCACCTGCTC
Oy      619 CTGCTCCGCTCAA 631
Db      631 CTGCTCCGCTCAA 643

```

RESULT 10
Bg762467 830 bp mRNA linear EST 15-MAY-2001
LOCUS 602733911F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4859138 5',
DEFINITION mRNA sequence.
ACCESSION Bg762467
VERSION Bg762467.1 GI:14073120
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 830)
TITLE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: InCyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM1714 row: F column: 03
 High quality sequence stop: 802.

FEATURES
 source
 1. 830
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4859138"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_49"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

Query Match 49.0%; Score 611; DB 2; Length 830;
 Best Local Similarity 100.0%; Pred. No. 9.9e-293;
 Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

51 GGTGGGCCCCGGGGGTAGAGCTCCAGAAAGGCGCATTTCTGAGATTGGCC 110
 59 GGTGGGCCCCGGGGGTAGAGCTCCAGAAAGGCGCATTTCTGAGATTGGCC 118
 111 ATCAGCCCCCATTTCTCTCTCAAAACCTGGTCAGAGGCGATGTTCCCTCATGGACCTTAA 170
 119 ATCAGCCCCCATTTCTCTCTCAAAACCTGGTCAGAGGCGATGTTCCCTCATGGACCTTAA 178
 171 AGACAGTGGCAAGTGGCTGCAACCGTGGACCAAGCCGACCACTGGGCGCGGTGATGG 230
 179 AGACAGTGGCAAGTGGCTGCAACCGTGGACCAAGCCGACCACTGGGCGCGGTGATGG 238
 231 TCCACGACGAGAGCGGTGGAGACCCCGCTCTCTGGGCGACGCTGTCTTAAGCTTGACAC 290
 239 TCCACGACGAGAGCGGTGGAGACCCCGCTCTCTGGGCGACGCTGTCTTAAGCTTGACAC 298
 291 CTGCAAGGCTGGAGACCACTGGATGGAGATCTCTGGGCGACGCTGTCTTAAGCTTGACAC 350
 299 CTGCAAGGCTGGAGACCACTGGATGGAGATCTCTGGGCGACGCTGTCTTAAGCTTGACAC 358
 351 GGAGGAAGAGAGAGAGGGGGCGGGGCGACCTTTGTCAGAGGGGCTTCCCGGCGAT 410
 359 GGAGGAAGAGAGAGAGGGGGCGGGGCGACCTTTGTCAGAGGGGCTTCCCGGCGAT 418
 411 GGGCTCTGAGAGATTGCGTCTGCTCTCTCTATGATGCGCGGCTGATGCTGAGGTGCC 470
 419 GGGCTCTGAGAGATTGCGTCTGCTCTCTCTATGATGCGCGGCTGATGCTGAGGTGCC 478
 471 ACCCGAGCTGCTGCTGCTGCTGCTGCTTTCTTCCACAGAGGCGCATAGGACAAAGTGAAGTG 530
 479 ACCCGAGCTGCTGCTGCTGCTGCTGCTTTCTTCCACAGAGGCGCATAGGACAAAGTGAAGTG 538
 531 CTTCCTTCTGCTATGAGGGGCTGACAGAGCTGGAAGGGGGGAGACACCCCTGAGAGAGCA 590
 539 CTTCCTTCTGCTATGAGGGGCTGACAGAGCTGGAAGGGGGGAGACACCCCTGAGAGAGCA 598
 591 TCCCAAGTGTTCCTCCAGCTGTCAAGTTCCTGCTCCGCTCAAAAGAGAGAGACTTTGTCCA 650
 599 TCCCAAGTGTTCCTCCAGCTGTCAAGTTCCTGCTCCGCTCAAAAGAGAGAGACTTTGTCCA 658
 651 CAGTGTGACAG 661
 |||||

Db 659 CAGTGTGACAG 669

RESULT 11
 BUI72109
 LOCUS
 DEFINITION
 AGENCOURT 7954295 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6109915
 5', mRNA sequence.
 ACCESSION
 BUI72109
 VERSION
 BUI72109.1 GI:22686093
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 956)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: gsa@b6-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM2356 row: I column: 20
 High quality sequence stop: 535.

FEATURES
 source
 1. 956
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6109915"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="NIH_MGC_112"
 /clone_lib="NIH_MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 48.6%; Score 606; DB 5; Length 956;
 Best Local Similarity 100.0%; Pred. No. 3.1e-290;
 Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

97 TTCTGAGATTGGCCATCAGCCCTTCTGCTGCAAACTGTGCAGAGGCGAGTTC 156
 1 TTCTGAGATTGGCCATCAGCCCTTCTGCTGCAAACTGTGCAGAGGCGAGTTC 160
 157 TCCATGGAGACCTTAAAGAGAGTGGCTGCAACCGTGGACCAAGCCGAGCACTGG 216
 61 TCCATGGAGACCTTAAAGAGAGTGGCTGCAACCGTGGACCAAGCCGAGCACTGG 120
 217 GCAGCCGAGTGAATGTCACGACGAGAGGCTGTGACCCCGCTCTTGGGCGAGCCCTGTC 276
 121 GCAGCCGAGTGAATGTCACGACGAGAGGCTGTGACCCCGCTCTTGGGCGAGCCCTGTC 180
 277 CTAGGCTGAGACACTGACAGGCTGTGAGACCACTGTGATGGGAGAGATCTTGGGCGAGCTG 336
 181 CTAGGCTGAGACACTGACAGGCTGTGAGACCACTGTGATGGGAGAGATCTTGGGCGAGCTG 240
 337 CGGCCCTGACAGAGAGAGAGAGAGAGAGGCGCGGGGCGACCTTGTCCAGGGGCGCT 396
 241 CGGCCCTGACAGAGAGAGAGAGAGAGAGGCGCGGGGCGACCTTGTCCAGGGGCGCT 300
 |||||

Oy 397 GCCTTCCCCGGATAGGGCTCTGAGAGTTCGCTTCGCGCTCTTCTATGACTCGGCCCTG 456
 Db 301 GCCTTCCCCGGATAGGGCTCTGAGAGTTCGCTTCGCGCTCTTCTATGACTCGGCCCTG 360
 Oy 457 ACTGCTGAGTGCACACCGAGCTGTGCGCTGTGCACGCGCTTCTTCCACACAGGCCATCAG 516
 Db 361 ACTGCTGAGTGCACACCGAGCTGTGCGCTGTGCACGCGCTTCTTCCACACAGGCCATCAG 420
 Oy 517 GACAAAGTGAGGTGCTTCTTCTGCTATGGGGGCTGCAGAGCTGGAAGGCCGGGAGCAGC 576
 Db 421 GACAAAGTGAGGTGCTTCTTCTGCTATGGGGGCTGCAGAGCTGGAAGGCCGGGAGCAGC 480
 Oy 577 CCTCTGAGACGAGCATGCCAAGTGGTTCCTCCAGCTGTCAATTCTTGCTCCGGTCAAAAGGA 636
 Db 481 CCTCTGAGACGAGCATGCCAAGTGGTTCCTCCAGCTGTCAATTCTTGCTCCGGTCAAAAGGA 540
 Oy 637 AGAGACTTGTTCACAGTGTGACGAGGACTCATCCAGCTGCTGGGCTCCCTGGGAGACCG 696
 Db 541 AGAGACTTGTTCACAGTGTGACGAGGACTCATCCAGCTGCTGGGCTCCCTGGGAGACCG 600
 Oy 697 TGGGAA 702
 Db 601 TGGGAA 606

RESULT 12	
BQ877438	
LOCUS	870 bp mRNA linear EST 16-AUG-2001
DEFINITION	AGNCOURT 8042576 NIH_MGC_112 Homo sapiens CDNA IMAGE:6090222
ACCESSION	5', mRNA sequence.
	BQ877438

Accession	B0877438	GI:22269446
Version	B0877438.1	
Keywords	EST	
Source	Homo sapiens	(human)
Organism	Homo sapiens	

REFERENCE	1 (bases 1 to 870)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

```

Plate: LLCM2331   row: e   column: 07
High quality sequence stop: 580.
Location/Qualifiers

```

```

source
1. .8/0
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6090223"
/tissue_type="melanotic melanoma, cell line"
/lab_host="RD10B (phage-resistant)"
/clone_idb="NIH_MGC_112"
/name="Organ; Skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

```

Query Match	47.6%	Score 593;	DB 5;	Length 870;
Best Local Similarity	100.0%	Pred. No. 9.3e-284;		
Matches 593; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	97	TTCTGAGTWTGGCCATCAGCCCCCATTTCTCTCTGCAAACTGGTCCAGGCGCATGTCC	156
Db	1	TTCTGAGATTGGCCATCAGCCCCCATTTCTCTCTGCAAACTGGTCCAGGCGCATGTTC	60
OY	157	TCGATGGGACCTTAAGAAGTGGCCAGTGCCTGACCGTGGACCAACAGCCAGCCACTGG	216
Db	61	TCGATGGGACCTTAAGAAGTGGCCAGTGCCTGACCGTGGACCAACAGCCAGCCACTGG	120
OY	217	GCAGCCGCTGATGGTCCGACGACGAGCGCTGTGGAACCCGCTCTCTTGGGCAGCCCTGTG	276
Db	121	GCAGCCGCTGATGGTCCGACGACGAGCGCTGTGGAACCCGCTCTCTTGGGCAGCCCTGTG	180
OY	277	CTAGGCGCTGGACACTGTGAGAGCTTGGGACCAAGTGGATGGGAGATCTTGGGCGCAGTG	336
Db	181	CTAGGCGCTGGACACTGTGAGAGCTTGGGACCAAGTGGAGATCTTGGGCGCAGTG	240
OY	337	CGGCCCTCTGACAGAGAGAGAGAGAGAGGAGCGCCCGGGGCGACCTTGTCCAGGGGGCT	396
Db	241	CGGCCCTCTGACAGAGAGAGAGAGAGAGGAGCGCCCGGGGCGACCTTGTCCAGGGGGCT	300
OY	397	GCCTTCCCCTGGCATGGGCTCTGAGGAGTTGGCTTGGCTCTCTCTTATGACTGGGCGCTG	456
Db	301	GCCTTCCCCTGGCATGGGCTCTGAGGAGTTGGCTTGGCTCTCTCTTATGACTGGGCGCTG	360
OY	457	ACTGCTGAGGTGGCCACCCGAGCTGTGGGCTGTGGGCTTCTTCCACAGAGGCATCAG	516
Db	361	ACTGCTGAGGTGGCCACCCGAGCTGTGGGCTGTGGGCTTCTTCTTCCACAGAGGCATCAG	420
OY	517	GACAAAGTGAAGTGTCTTCTCTGCTATGGGGGCTGTGAGAGCTGGAAGCGGGGGACGAC	576
Db	421	GACAAAGTGAAGTGTCTTCTCTGCTATGGGGGCTGTGAGAGCTGGAAGCGGGGGACGAC	480
OY	577	CCCTTGGACGAGCATGCCAAGTGGTTCCTCCAGCTGTCAATTCCTGTCTCCGATCAAAAGGA	636
Db	481	CCCTTGGACGAGCATGCCAAGTGGTTCCTCCAGCTGTCAATTCCTGTCTCCGATCAAAAGGA	540
OY	637	AGAGACTTTTGTCCACAGTGTGCAGAGAGCTCACTCCAGAGTGCTGGGCTCTCTG	689
Db	541	AGAGACTTTTGTCCACAGTGTGCAGAGAGCTCACTCCAGAGTGCTGGGCTCTCTG	593

RESULT 13	
LOCUS	BO877652
DEFINITION	BO877652 919 bp mRNA linear EST 16-AUG-2002
ACCESSION	AGNCOCURT_8095636 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6087865
VERSION	BO877652
KEYWORDS	5', mRNA sequence.
SOURCE	BO877652.1 GI:2269660
ORGANISM	EST.
	Homo sapiens (human)
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 919)	NIH-MGC	http://mgc.nci.nih.gov/		
	National Institutes of Health,	Mammalian Gene Collection (MGC)		
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgabbs-remail.nih.gov			
	Tissue Procurement: DCTD/DRP			
	CDNA Library Preparation: Rubin Laboratory			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNL at:			
	http://image.llnl.gov			
	Plate: LHCW325	row: c	column: 06	
	High quality sequence stop: 604.			

FEATURES

Location/Qualifiers
1..919
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6087869"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA Synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 47.4%; Score 593; DB 5; Length 919;
Best Local Similarity 100.0%; Pred. No. 9.3e-284; Mismatches 0; Indels 0; Gaps 0;
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 97 TTCTGAGATTGGCCATAGCCCCCATTTCTGCTGCAAACTGTGTAGAGCCAGTGTCCC 156
Db 1 TTCTGAGATTGGCCATAGCCCCCATTTCTGCTGCAAACTGTGTAGAGCCAGTGTCCC 60
OY 157 TCCATGGGACCTTAAGACAGTGGCCAGTGGCTGTGACCCGCTCTCTGGGACAGCCCTG 216
Db 61 TCCATGGGACCTTAAGACAGTGGCCAGTGGCTGTGACCCGCTCTCTGGGACAGCCCTG 120
OY 217 GCACCCGGTATGTCTCCACGACAGAGCGGTGTGACCCGCTCTCTGGGACAGCCCTG 276
Db 121 GCACCCGGTATGTCTCCACGACAGAGCGGTGTGACCCGCTCTCTGGGACAGCCCTG 180
OY 277 CTAGGCTGTGACAGCTGTGACAGCTGTGACAGCTGTGACAGCTGTGACAGCTGTG 336
Db 181 CTAGGCTGTGACAGCTGTGACAGCTGTGACAGCTGTGACAGCTGTGACAGCTGTG 240
OY 337 CGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396
Db 241 CGGCCCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
OY 397 GCCCTCCCGGCGATGGGCTGTGAGAGAGTTCGCTGTGAGCTCTCTTATGACTGAC 456
Db 301 GCCCTCCCGGCGATGGGCTGTGAGAGAGTTCGCTGTGAGCTCTCTTATGACTGAC 360
OY 457 ACTGCTGAGGTGCACCCGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 516
Db 361 ACTGCTGAGGTGCACCCGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 420
OY 517 GACAAGTATAGTCTTCTTCTGCTATGAGGGGCTGTGACAGAGCTGTGACAGAGCTG 576
Db 421 GACAAGTATAGTCTTCTTCTGCTATGAGGGGCTGTGACAGAGCTGTGACAGAGCTG 480
OY 577 CCTGTGACGAGAGATGCCAAGTGTTCCTCCAGCTGTGACAGTCTCTCCGTCAAAGA 636
Db 481 CCTGTGACGAGAGATGCCAAGTGTTCCTCCAGCTGTGACAGTCTCTCCGTCAAAGA 540
OY 637 AAGAGCTTGTGTCAAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTGCT 689
Db 541 AAGAGCTTGTGTCAAGTGTGACAGAGACTCACTCCAGCTGTGAGGCTCTGCT 593
```

RESULT 14
Bg763730 652 bp mRNA linear EST 15-MAY-2001
LOCUS Bg763730
DEFINITION 60235757p1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4860951 5',
mRNA sequence.
ACCESSION Bg763730
VERSION Bg763730.1 GI:14074383
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 652)
REFERENCE
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L16M1719 row: a column: 16
High quality sequence stop: 650.

FEATURES

source

Location/Qualifiers
1..652
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4860951"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.0kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 47.4%; Score 591; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 9.1e-283; Mismatches 0; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 51 GGTGGGCCCCGGGGGTCAGAGAGTCTCAAGAGGCCAGTGGCATATTTCTGAGATTGGCC 110
Db 62 GGTGGGCCCCGGGGGTCAGAGAGTCTCAAGAGGCCAGTGGCATATTTCTGAGATTGGCC 121
OY 111 ATCAGCCCCCATTTCTGCTGCAAACTGTGTGACAGCGAGTTCCTCCATGGGACCTTAA 170
Db 122 ATCAGCCCCCATTTCTGCTGCAAACTGTGTGACAGCGAGTTCCTCCATGGGACCTTAA 181
OY 171 AGACAGTGCAGAGTGTGTGACAGCTGTGACAGAGCCAGAGCTGTGGAGCGGAGTAG 230
Db 182 AGACAGTGCAGAGTGTGTGACAGCTGTGACAGAGCCAGAGCTGTGGAGCGGAGTAG 241
OY 231 TCCACAGCAGAGCGCTGTGACCCCGGCTCTGTGGGAGAGCCCTGTCTTGAAGCTTGA 290
Db 242 TCCACAGCAGAGCGCTGTGACCCCGGCTCTGTGGGAGAGCCCTGTCTTGAAGCTTGA 301
OY 291 CTGCAAGAGCTTGGAGCAAGTGTGATGGCAGATCTGTGGGCCAGTGTGGCCCTGACAGA 350
Db 302 CTGCAAGAGCTTGGAGCAAGTGTGATGGCAGATCTGTGGGCCAGTGTGGCCCTGACAGA 361
OY 351 GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 410
Db 362 GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
OY 411 GGGCTTCTGAGAGAGTTCGCTGTGAGCTCTTCTATGACTGAGCCGCTGACTGAGTGGCC 470
Db 422 GGGCTTCTGAGAGAGTTCGCTGTGAGCTCTTCTATGACTGAGCCGCTGACTGAGTGGCC 481
OY 471 ACCGAGGTGTGCTGTGCTGTGCGGCTTCTTTCACACAGGCCATCAGAGCAAGGTGAGGTG 530
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 22, 2006, 09:16:51 ; Search time 262 Seconds
(without alignments)
8453.595 Million cell updates/sec

Title: US-09-762-577B-11
Perfect score: 1246
Sequence: 1 CGCAGCAGGAGCCGTCGCGG.....AGTCGCTTCCTCGAGGCT 1246

Sequences: 1303057 seqs, 888780828 residues
Gapop 60.0, Gapept 60.0

Total number of hits satisfying chosen parameters: 2605320

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6H_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCRTUS_COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PC_COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1177	94.5	1260	3	US-09-949-016-1949 Sequence 1949, App1
2	742	59.6	1337	3	US-09-127-928-1 Sequence 1, App1
3	491	39.4	8572	3	US-09-949-016-13691 Sequence 13691, A
4	203	16.3	601	3	US-09-949-016-66130 Sequence 66130, A
5	175	14.0	601	3	US-09-949-016-66140 Sequence 66140, A
6	168	13.5	226	3	US-09-023-655-334 Sequence 334, App
7	147	11.8	601	3	US-09-949-016-66139 Sequence 66139, A
8	103	8.3	601	3	US-09-949-016-66134 Sequence 66134, A
9	94	7.5	200	3	US-09-016-434-216 Sequence 216, App
10	94	7.5	200	3	US-09-023-655-387 Sequence 387, App
11	87	7.0	601	3	US-09-949-016-66138 Sequence 66138, A
12	82	6.6	601	3	US-09-949-016-66133 Sequence 66133, A
13	81	6.5	601	3	US-09-949-016-66135 Sequence 66135, A
14	81	6.5	601	3	US-09-949-016-66136 Sequence 66136, A
15	74	5.9	601	3	US-09-949-016-66137 Sequence 66137, A
16	44	3.5	601	3	US-09-949-016-66141 Sequence 66141, A
17	25	2.0	25	3	US-09-127-928-4 Sequence 4, App1
18	25	2.0	25	3	US-09-127-928-5 Sequence 5, App1
19	24	1.9	24	3	US-09-127-928-7 Sequence 7, App1
20	24	1.9	27	3	US-09-127-928-3 Sequence 3, App1
21	22	1.8	2699	3	US-10-104-047-800 Sequence 800, App
22	22	1.8	6649	3	US-09-799-451-384 Sequence 384, App
23	21	1.7	21	3	US-09-127-928-6 Sequence 6, App1
24	21	1.7	601	3	US-09-949-016-91698 Sequence 91698, A

25	21	1.7	601	3	US-09-949-016-91699	A	Sequence 91699, A
26	21	1.7	601	3	US-09-949-016-194639		Sequence 194639, A
27	21	1.7	601	3	US-09-949-016-194640		Sequence 194640, A
28	21	1.7	601	3	US-09-949-002-6005		Sequence 6005, App
29	21	1.7	601	3	US-09-949-002-6006		Sequence 6006, App
30	21	1.7	601	3	US-09-949-002-10069		Sequence 10069, A
31	21	1.7	601	3	US-09-949-002-10070		Sequence 10070, A
32	21	1.7	3121	3	US-10-033-301-6		Sequence 6, App1
33	21	1.7	36075	3	US-09-949-016-16571		Sequence 16571, A
34	21	1.7	36075	3	US-09-949-016-16572		Sequence 16572, A
35	21	1.7	36625	3	US-09-949-016-12788		Sequence 12788, A
36	21	1.7	37133	3	US-09-949-016-16569		Sequence 16569, A
37	21	1.7	37133	3	US-09-949-016-16570		Sequence 16570, A
38	21	1.7	197336	3	US-09-949-016-12881		Sequence 12881, A
39	21	1.7	197337	3	US-09-949-016-14376		Sequence 14376, A
40	21	1.7	197337	3	US-09-949-002-738		Sequence 738, App
41	21	1.7	234287	3	US-09-949-002-687		Sequence 687, App
42	21	1.7	234288	3	US-09-949-016-17272		Sequence 17272, A
43	21	1.7	234288	3	US-09-949-002-841		Sequence 841, App
44	20	1.6	319	3	US-09-513-999C-31552		Sequence 31552, A
45	20	1.6	601	3	US-09-949-016-109502		Sequence 109502, A

ALIGNMENTS

RESULT 1
US-09-949-016-1949
Sequence 1949, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1949
LENGTH: 1260
TYPE: DNA
ORGANISM: Human
US-09-949-016-1949
Query Match 94.5%; Score 1177; DB 3; Length 1260;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
19 GGCAGGCTGCTGCTATTCCTGCTGCTCCAGAGGTGGGCCCCGGGGGTCAAGACTTCAG 78
|||||
79 AAGGGCCAGTGGGCAATTCAGATTCGACATTCACCCCAATTCGTCGCAAACTG 138
|||||
93 AAGGGCCAGTGGGCAATTCGATTCGACATTCACCCCAATTCGTCGCAAACTG 152
|||||
139 GTCAGAGCCAGTGTTCCTCCATGAGGACCTTAAGACAGTGCCTCAAGTCTGCAACCTG 198
|||||
153 GTCAGAGCCAGTGTTCCTCCATGAGGACCTTAAGACAGTGCCTCAAGTCTGCAACCTG 212
|||||
199 CCACAGCCGAGCCACTGCGGAGCCGAGTGTTCCTCCAGAGGAGCCCTGTGACACCCCG 258
|||||
213 CCACAGCCGAGCCACTGCGGAGCCGAGTGTTCCTCCAGAGGAGCCCTGTGACACCCCG 272
|||||
259 TCTGTGGAGCCCTGCTAGGCTGAGACCTGAGAGCCCTGAGACCAAGTGTGAGG 318
|||||

Db	273	TTCTTGGGAGACCCCTGTCTTAAGGCTTGACACTCTGCAGAGCCTGGAGCAACAGTGGATGG	332
QY	319	CAGATCTCTGGGACGACTGGCGGCCCTTGACAGAGGAGGAAGAGAGAGGCGCGGAGGC	378
Db	333	CAGATCTCTGGGACGACTGGCGGCCCTTGACAGAGGAGGAAGAGAGAGGCGCGGAGGC	392
QY	379	ACCTTGTCCAGGGGGGCTGCGCTTCCCGGGATGGGGCTGTAGAGATTGCGTTCGCTCC	438
Db	393	ACCTGTGCCAGGGGGGCTGCGCTTCCCGGGATGGGCTCTAGAGAGTTGCGTTCGCTCC	452
QY	439	TTCTATGACTGCGCGCTGACTGCTGAGGTGCACCCGAGCTGCTGCTGCGCGCTTC	498
Db	453	TTCTATGACTGCGCGCTGACTGCTGAGGTGCACCCGAGCTGCTGCTGCGCGCTTC	512
QY	499	TTCCACAGAGGCCATCAGACCAAGAGAGGTGCTTCTTGTGCTATAGGGGCTTCGAGAGC	558
Db	513	TTCCACAGAGGCCATCAGACCAAGAGAGGTGCTTCTTGTGCTATAGGGGCTTCGAGAGC	572
QY	559	TGGAAAGCGGGGAGCAACCCCTGAGCGAGCATGCCAAGTGTTTCCCACTGTCACTTC	618
Db	573	TGGAAAGCGGGGAGCAACCCCTGAGCGAGCATGCCAAGTGTTTCCCACTGTCACTTC	632
QY	619	CTGCTCCGGTCAAAAAGAAAGAGCTTTGTCCACAGTGTGAGAGACTACTTCCAGCTG	678
Db	633	CTGCTCCGGTCAAAAAGAAAGAGCTTTGTCCACAGTGTGAGAGACTACTTCCAGCTG	692
QY	679	CTGGGCTCCTGGAGCCCGTGGAGAAAGCCGGAAGACGACGCCCTGTGGCCCCCTCCGTC	738
Db	693	CTGGGCTCCTGGAGCCCGTGGAGAAAGCCGGAAGACGACGCCCTGTGGCCCCCTCCGTC	752
QY	739	CTTGCCCTTGGGGTACCCTGAGCTGCCCAACCCAGAGAGAGTCCAGTCTAAAGTGC	798
Db	753	CTTGCCCTTGGGGTACCCTGAGCTGCCCAACCCAGAGAGAGTCCAGTCTAAAGTGC	812
QY	799	CAGAGGCCAGAGGCCAGGAGTGTGAGAGCGCAGCTGCGCGGCTGCAGAGAGAGAGAC	858
Db	813	CAGAGGCCAGAGGCCAGGAGTGTGAGAGCGCAGCTGCGCGGCTGCAGAGAGAGAGAC	872
QY	859	TGCAAGGTGTGCTGGACCGCGGCCGCTGTCCATCGTCTTTGTGCGGTGCGGCCACTTGTC	918
Db	873	TGCAAGGTGTGCTGGACCGCGGCCGCTGTCCATCGTCTTTGTGCGGTGCGGCCACTTGTC	932
QY	919	TGTGCTGAGTGTGCCGCCCGGCTGAGCTGTGCCCATCTGCAGAGCCCGGCTCGAGC	978
Db	933	TGTGCTGAGTGTGCCGCCCGGCTGAGCTGTGCCCATCTGCAGAGCCCGGCTCGAGC	992
QY	979	CGCGTGCCGCACTTCTGTGCTCTTAGGCCAGGTGCCATGCGCGGCCAGGTGGGCTGCAGAGT	1038
Db	993	CGCGTGCCGCACTTCTGTGCTCTTAGGCCAGGTGCCATGCGCGGCCAGGTGGGCTGCAGAGT	1052
QY	1039	GAGGCTCCCTGCCCCCTCTGTGCTGTTCTGCACTGTGTTCTGGGGCTGCTGAGAGATGGAG	1098
Db	1053	GAGGCTCCCTGCCCCCTCTGTGCTGTTCTGCACTGTGTTCTGGGGCTGCTGAGAGATGGAG	1112
QY	1099	AGCTGTGTTCATCCAGACTGACATCAGGCCCTGATTCCCGACCAACCGCCAGGGTGGAGA	1158
Db	1113	AGCTGTGTTCATCCAGACTGACATCAGGCCCTGATTCCCGACCAACCGCCAGGGTGGAGA	1172
QY	1159	AGAGAGCCCTTGTGTGGCGTGGGGAGATGGCTTAATGATCACTGTTGGATGCTTCTGAAT	1218
Db	1173	AGAGAGCCCTTGTGTGGCGTGGGGAGATGGCTTAATGATCACTGTTGGATGCTTCTGAAT	1232
QY	1219	AGAAATAAGTGGGTTTTTCTCTTGGAGGT	1246
Db	1233	AGAAATAAGTGGGTTTTTCTCTTGGAGGT	1260

```

? APPLICANT: Lin, Jiling-Huey
? APPLICANT: Morser, Michael J
? TITLE OF INVENTION: DNA Encoding a No. 6472172e1 Human Inhibitor-of-Apoptosis
? TITLE OF INVENTION: Protein
? FILE REFERENCE: DNA Encoding HIAP3
? CURRENT APPLICATION NUMBER: US/09/127,928
? CURRENT FILING DATE: 1998-07-31
? NUMBER OF SEQ. ID NOS: 7
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1
? LENGTH: 1337
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (170)..(1066)
? US-09-127-928-1

```

Query Match	Similarity	Score	DB 3	Length
Best Local	99.9%	742	1337	
Matches	752	Conservative	0	MisMatches
			1	Indels
			0	Gaps
			0	
QY	19	GGCAGGCGCTGAGCCATATCCCTGCTGTGCTCCCAAGGATGGGCGGGGGGTACAGAGCTCCAG	78	
Db	29	GGCAGGCGCTGAGCCATATCCCTGCTGTGCTCCCAAGGATGGGCGGGGGGTACAGAGCTCCAG	88	
QY	79	AAGGGCCACGCTGGGGCATATTTCTGATTTGGCATTCAGCCCCCATTTCTGCTGCAACCTG	138	
Db	89	AAGGGCCACGCTGGGGCATATTTCTGATTTGGCATTCAGCCCCCATTTCTGCTGCAACCTG	148	
QY	139	GTCCAGAGCCAGTGTTCCTCCATAGGGGACCTAAAGACAGTGGCCACAGTGCCTGCACCTGGA	198	
Db	149	GTCCAGAGCCAGTGTTCCTCCATAGGGGACCTAAAGACAGTGGCCACAGTGCCTGCACCTGGA	208	
QY	199	CCACAGCCGGAACCATGAGGAGCGCGGTGATGTGCCACGAGAGGCGCTGTGACCCCCG	258	
Db	209	CCACAGCCGGAACCATGAGGAGCGCGGTGATGTGCCACGAGAGGCGCTGTGACCCCCG	268	
QY	259	TCTCTGGGGCAGCCCTGTCTTAGGCTGTGACACTTGACAGCCTTGAGCCACGCTGATGGG	318	
Db	269	TCTCTGGGGCAGCCCTGTCTTAGGCTGTGACACTTGACAGCCTTGAGCCACGCTGATGGG	328	
QY	319	CAGATCCTGGAGCCAGCTGCGGCGCCCTGACAGAGAGAGAGAGAGAGGCGCCGGGCGC	378	
Db	329	CAGATCCTGGAGCCAGCTGCGGCGCCCTGACAGAGAGAGAGAGAGAGGCGCCGGGCGC	388	
QY	379	ACCTTGTCCAGGGGGCGCTGCTTCCCGGACATGGGCTCTGAGAGATTGCGTGTGCGCTCC	438	
Db	389	ACCTTGTCCAGGGGGCGCTGCTTCCCGGACATGGGCTCTGAGAGATTGCGTGTGCGCTCC	448	
QY	439	TTCTATATACCTGGGCGCGCTGACTGTGAGGTGGCCACCCGAGCTGTGGCTGCGCGCTTC	498	
Db	449	TTCTATATACCTGGGCGCGCTGACTGTGAGGTGGCCACCCGAGCTGTGGCTGCGCGCTTC	508	
QY	499	TTCCACACAGGCCCATCAGACAAAGGTGAGGTCTTCTTCTGCTATGAGGGGCGCTGAGGC	558	
Db	509	TTCCACACAGGCCCATCAGACAAAGGTGAGGTCTTCTTCTGCTATGAGGGGCGCTGAGGC	568	
QY	559	TGGAAGCGCGGGGACGACCCCTTGAGCGAGCATGCGCAAGTGGTTCCCGAGCTGTCACTTC	618	
Db	569	TGGAAGCGCGGGGACGACCCCTTGAGCGAGCATGCGCAAGTGGTTCCCGAGCTGTCACTTC	628	
QY	619	CTGCTCCGGGTCAAAAGAGAGACTTTGTGCCAATGTGGCAGAGACTCATCTCCAGCTG	678	
Db	629	CTGCTCCGGGTCAAAAGAGAGACTTTGTGCCAATGTGGCAGAGACTCATCTCCAGCTG	688	
QY	679	CTGGGGCTCTTGGGACCCGCTGGAGAAACCGGAAACGACGCCCTGTGGACCCCTCCGTC	738	
Db	689	CTGGGGCTCTTGGGACCCGCTGGGAAACCGGAAACGACGCCCTGTGGACCCCTCCGTC	748	
QY	739	CTGGCTCTTGGGATCCCTGAGCTGCCACACCCAGAGAGAGGTTCACGTCTGAAAGTGC	798	
Db	749	CTGGCTCTTGGGATCCCTGAGCTGCCACACCCAGAGAGAGGTTCACGTCTGAAAGTGC	808	

OY 799 CAGAGCCAGAG 811
Db 809 CAGAGCCAGAG 821

RESULT 3

US-09-949-016-13691
Sequence 13691, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13691
LENGTH: 8572
TYPE: DNA
ORGANISM: Human
US-09-949-016-13691

Query Match 39.4%; Score 491; DB 3; Length 8572;
Best Local Similarity 100.0%; Pred. No. 2,4e-212;

Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 GGCAGGCGCTGTCCTATCCCTGCTGTCCTCCAGGGGGGCGGGGGGTCAGAGCTCCAG 78
Db 2033 GGCAGGCGCTGTCCTATCCCTGCTGTCCTCCAGGGGGGCGGGGGGTCAGAGCTCCAG 2092
OY 79 AAGGGCCAGCTGGGCAATATTCGATTTGGCCATCAGCCCATTTCTGCTGCAAACTG 138
Db 2093 AAGGGCCAGCTGGGCAATATTCGATTTGGCCATCAGCCCATTTCTGCTGCAAACTG 2152
OY 139 GTCAGAGCAGTGTTCCTTCATGAGAGCTTAAAGACAGTCCAAAGTCTGCACCTGGA 198
Db 2153 GTCAGAGCAGTGTTCCTTCATGAGAGCTTAAAGACAGTCCAAAGTCTGCACCTGGA 2212
OY 199 CCAGAGCCGAGCACTGGGCGAGCGGTGATGTCCCAAGAGAGCGCTGAGACCCCGC 258
Db 2213 CCAGAGCCGAGCACTGGGCGAGCGGTGATGTCCCAAGAGAGCGCTGAGACCCCGC 2272
OY 259 TCTGTGGGAGCCCTGTCTCTAGAGCTTGACACTGACAGAGCTGGGACCACTGATGGG 318
Db 2273 TCTGTGGGAGCCCTGTCTCTAGAGCTTGACACTGACAGAGCTGGGACCACTGATGGG 2332
OY 319 CAGATCTGGGCGCAGCTGCGGCGCTTGAACAAGAGAGAGAGGCGCGGGGCGC 378
Db 2333 CAGATCTGGGCGCAGCTGCGGCGCTTGAACAAGAGAGAGAGGCGCGGGGCGC 2392
OY 379 ACCTGTTCAGAGGGGCGCTGCTCCCGGAGATGGGCTGAGAGATTGCGTGGCCCTCC 438
Db 2393 ACCTGTTCAGAGGGGCGCTGCTCCCGGAGATGGGCTGAGAGATTGCGTGGCCCTCC 2452
OY 439 TTCTATGACTGGCGCTGACTGCTGAGGTGCCACCCGAGCTGCTGCTGCGCGCTTC 498
Db 2453 TTCTATGACTGGCGCTGACTGCTGAGGTGCCACCCGAGCTGCTGCTGCGCGCTTC 2512
OY 499 TTCCACACAGG 509
Db 2513 TTCCACACAGG 2523

RESULT 4

US-09-949-016-66130
Sequence 66130, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66130
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-66130

Query Match 16.3%; Score 203; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 5,4e-82;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 307 CAGGTGATGGGAGATCTGGGCGCAGCTGGGCGCCCTGACAGAGAGAGAGAGAGAG 366
Db 1 CAGGTGATGGGAGATCTGGGCGCAGCTGGGCGCCCTGACAGAGAGAGAGAGAGAG 60
OY 367 GCGCGCGGCGCCACCTTGTCCAGGGGCGCTGCTCCCGCATGGGCTGTGAGAGATTG 426
Db 61 GCGCGCGGCGCCACCTTGTCCAGGGGCGCTGCTCCCGCATGGGCTGTGAGAGATTG 120
OY 427 CGTGTGCTCTCTTATGACTGGCGCGCTGACTGCTAGGTGCCACCCGAGCTGCTGCT 486
Db 121 CGTGTGCTCTCTTATGACTGGCGCGCTGACTGCTAGGTGCCACCCGAGCTGCTGCT 180
OY 487 GCTGCGGCGCTTCTCCACAGAG 509
Db 181 GCTGCGGCGCTTCTCCACAGAG 203

RESULT 5

US-09-949-016-66140
Sequence 66140, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66140
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-66140

Query Match 14.0%; Score 175; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2,5e-69;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 US-09-949-016-66134
 Sequence 66134, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: C1001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 66134

LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-66134

Query Match 8.3%; Score 103; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 9.7e-37;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CAGCCATCAGACAGAGTGAAGTCTTCTGCTATGAGGAGCTGAGAGCTGGAAGC 565
DB 330 CAGCCATCAGACAGAGTGAAGTCTTCTGCTATGAGGAGCTGAGAGCTGGAAGC 389
QY 566 GCGGGAGACAGCCCTTGGAGAGGAGCATGCCAAGTGTCTCCCAAG 608
DB 390 GCGGGAGACAGCCCTTGGAGAGGAGCATGCCAAGTGTCTCCCAAG 432

RESULT 9

US-09-016-434-216
Sequence 216, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADTUT04
CLONE: 1520835
US-09-016-434-216

Query Match 7.5%; Score 94; DB 3; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 TCGCGCGCTGCAGAGAGAGAGAGAGTGTGCTGACCGCGCTGTGCATCG 892
DB 38 TCGCGCGCTGCAGAGAGAGAGAGAGTGTGCTGACCGCGCTGTGCATCG 97

QY 893 TCTTTGCGCGTGCAGAGAGAGAGAGTGTGCTGACCGCGCTGTGCATCGA 926
DB 98 TCTTTGCGCGTGCAGAGAGAGAGAGTGTGCTGACCGCGCTGTGCATCGA 131

RESULT 10

US-09-023-655-387
Sequence 387, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 387:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADTUT04
CLONE: 1520835
US-09-023-655-387

Query Match 7.5%; Score 94; DB 3; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 TCGCGCGCTGCAGAGAGAGAGAGTGTGCTGACCGCGCGCTGTGCATCG 892
DB 38 TCGCGCGCTGCAGAGAGAGAGAGTGTGCTGACCGCGCGCTGTGCATCG 97
QY 893 TCTTTGCGCGTGCAGAGAGAGAGAGTGTGCTGACCGCGCTGTGCATCGA 926
DB 98 TCTTTGCGCGTGCAGAGAGAGAGAGTGTGCTGACCGCGCTGTGCATCGA 131

RESULT 11
US-09-949-016-66138
Sequence 66138, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

```

? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: C0001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ. ID NOS: 207012
? SOFTWARE: PARSSEQ for Windows Version 4.0
? SEQ. ID NO 66138
? LENGTH: 601
? TYPE: DNA
? ORGANISM: Human
? US-09-949-016-66138

```

```
Query Match      7.0%; Score 87; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e-29;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY	805	CCGAGGACCGAGGATATGTGGAGGCGCAGCTGCGCGCGCTGACGAGAGAGAGACCTGCAAG	864
Db	515	CCAGAGCCAGGATATGTGGAGGCGCAGCTGCGCGCGCTGACGAGAGAGAGACCTGCAAG	574
QY	865	GTTGTGCTGAGACCGCGCCCTGTTCATTC	891
Db	575	GTTGTGCTGAGACCGCGCCCTGTTCATTC	601

```

RESULT 12
US-09-949-016-66131
; Sequence 66131, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66131
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66131

```

Query Match	6.6%	Score 82;	DB 3;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 3.1e-27;		
Matches 82;	Conservative 0;	Mismatches 0;	Inserts 0;	Deletions 0;

Qy	428	GTCGACCCCTCTTATATACATGCGCGCTGATCTGCTAGAGGTGCCACCCGAGCTGCTGG	487
Db	1	GCTGCGCCTCTTATATACATGCGCGCTGACTGCTAGAGGCCACCCGAGCTGCTGG	60
Qy	488	CTGCGCGCTCTTCCACACAG	509
Db	61	CTGCGCGCTTCTTCCACACAG	82

RESULT 13
US-09-949-016-66135

```

; Sequence 66135, Application US/09494016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 66135
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66135

```

Query Match	6.5%	Score 81;	DB 3;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 8.8e-27;		
Matches 81;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Accession	Sequence	Length
OY	606 CAGCTGTCACTTCTGTCCGGTCAAAAGAGACATTGTCCACACTGTGCGAGAC	66
Db	439 CAGCTGTCACTTCTGTCCGGTCAAAAGAGACATTGTCCACACTGTGCGAGAC	498
OY	666 TCACTCCCACTCTGGCTC	66
Db	499 TCACTCCCACTGTGGCTC	519

```

RESULT 14
US-09-949-016-66136
; Sequence 66136, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66136
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66136

```

```
Query Match      6.5%; Score 81; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 8.8e-27;
Matches      81; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY	600	CAGCTGTCA	GTCCGCTCCG	GTCAAAAG	GAAGAC	CTTTTGT	CCACAGTGTG	CAGAGAGAC	665
Db	220	CAGCTGTCA	GTTCCTCGCTCCG	GTCAAAAG	GAAGAC	CTTTTGT	CCACAGTGTG	CAGAGAGAC	279
QY	666	TCATCTCCA	GAGCTGCTGG	AGCTC	686				
Db	280	TCATCTCCA	GAGCTGCTGG	AGCTC	300				

RESULT 15

US-09-949-016-66137
; Sequence 66137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66137
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66137

Query Match

5.9%; Score 74; DB 3; Length 601;

Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	736	GTCCCTGCTGTGGGTACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGT	795
DB	349	GTCCCTGCTGTGGGTACCTGAGCTGCCACACCCAGAGAGAGTCCAGTCTGAAGT	408
QY	796	GCCGAGAGCCAGG	809
DB	409	GCCGAGAGCCAGG	422

Search completed: April 22, 2006, 11:04:17
Job time : 264 secs

THIS PAGE BLANK (USPTO)

Result No.	Score	Query Match	Length	DB	ID	Description
1	1228	98.6	1260	6	US-10-188-646-4	Sequence 4, Appl1
2	1228	98.6	1268	8	US-10-807-897-28	Sequence 28, Appl1
3	1228	98.6	1376	5	US-10-244-586-1	Sequence 1, Appl1
4	843	67.7	843	5	US-10-244-586-2	Sequence 2, Appl1
5	793	63.6	1322	8	US-10-807-897-26	Sequence 26, Appl1
6	742	59.6	1337	5	US-10-825-026-1	Sequence 1, Appl1
7	742	59.6	1363	8	US-10-839-882-37	Sequence 37, Appl1
8	638	51.2	858	8	US-10-723-860-8265	Sequence 8265, Appl1
9	601	48.2	1168	6	US-10-188-646-12	Sequence 12, Appl1
10	532	42.7	1068	6	US-10-203-708-21	Sequence 21, Appl1
11	491	39.4	481-1	6	US-10-188-646-11	Sequence 11, Appl1
12	449	35.0	449	8	US-10-723-860-4697	Sequence 4697, Appl1
13	447	35.0	769	6	US-10-203-708-22	Sequence 22, Appl1
14	439	35.2	676	8	US-10-723-860-4448	Sequence 4448, Appl1
15	366	29.4	3782	9	US-10-450-763-27357	Sequence 27357, Appl1
16	311	25.0	615	7	US-10-286-115-63	Sequence 63, Appl1
17	310	24.9	614	9	US-10-450-763-27354	Sequence 27354, Appl1
18	268	21.5	444	9	US-10-450-763-27355	Sequence 27355, Appl1
19	262	21.0	399	9	US-10-963-495-1	Sequence 1, Appl1
20	168	13.5	226	7	US-10-661-643-334	Sequence 334, Appl1
21	122	9.8	404	9	US-10-779-543-12365	Sequence 12365, Appl1
22	94	7.5	200	6	US-10-305-720-216	Sequence 216, Appl1
23	94	7.5	200	7	US-10-641-643-387	Sequence 387, Appl1

C 25	74	5	720	5	US-10-027-633-14213	A	Sequence 14213, A
C 24	74	5	720	5	US-10-027-633-14214	A	Sequence 14214, A
C 26	74	5	720	6	US-10-027-633-14213	A	Sequence 14213, A
C 27	74	5	720	6	US-10-027-633-14214	A	Sequence 14214, A
C 28	74	5	721	5	US-10-027-633-145092	A	Sequence 145092, A
C 29	74	5	721	6	US-10-027-633-145092	A	Sequence 145092, A
C 30	74	5	721	6	US-09-908-975-11312	A	Sequence 11312, A
C 31	74	5	698	5	US-10-027-633-145255	A	Sequence 145255, A
C 32	74	5	698	5	US-10-027-633-145256	A	Sequence 145256, A
C 33	74	5	698	5	US-10-027-633-145257	A	Sequence 145257, A
C 34	74	5	698	6	US-10-027-633-145255	A	Sequence 145255, A
C 35	74	5	698	6	US-10-027-633-145256	A	Sequence 145256, A
C 36	74	5	698	6	US-10-027-633-145257	A	Sequence 145257, A
C 37	74	5	27	6	US-10-188-646-7	A	Sequence 7, Appli
C 38	74	5	25	5	US-10-235-026-4	A	Sequence 4, Appli
C 39	74	5	25	5	US-10-235-026-5	A	Sequence 5, Appli
C 40	74	5	24	5	US-10-235-026-7	A	Sequence 7, Appli
C 41	74	5	27	5	US-10-235-026-3	A	Sequence 3, Appli
C 42	74	5	90650	5	US-10-175-523-80	A	Sequence 80, Appl
C 43	74	5	90650	10	US-11-099-266-80	A	Sequence 80, App
C 44	74	5	158	8	US-10-425-115-39519	A	Sequence 39519, A
C 45	74	5	432	7	US-10-424-599-126316	A	Sequence 126316, A

ALIGNMENTS

```

RESULT 1
US-10-188-646-4
; Sequence 4, Application US/10188646
; Publication NO. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1016)
; US-10-188-646-4

```

Query Match	98.6%	Score 1228;	DB 6;	Length 1260;
-------------	-------	-------------	-------	--------------

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

QY	31.9	CAGATCTTGAGCCAGCTGCGCCCTCTGA	CAGAGGAAAGAGAGAGCGCCGAGGCC	378
Db	33.3	CAGATCTTGAGCCAGCTGCGCCCTCTGA	CAGAGGAAAGAGAGAGCGCCGAGGCC	392
QY	37.9	ACCTTGTCAGAGGAGCGCTGCCCTTCCCGGCA	TGGGCTTGAGAGATTGCGTTCGCTCC	438
Db	39.3	ACCTTGTCAGAGGAGCGCTGCCCTTCCCGGCA	TGGGCTTGAGAGATTGCGTTCGCTCC	452
QY	43.9	TTCTATGACTGCGCGCTGACTGCTGAGAGTGC	CCCGAGCTGCTGCGCGCGCTTC	498
Db	45.3	TTCTATGACTGCGCGCTGACTGAGGTGC	CCCGAGCTGCTGCGCGCGCTTC	512
QY	49.9	TTTCACACAGGCGCATTCAGGACAAAGTGA	GGTCTTTCTGCTATGCGGCGCTTGACAGC	558
Db	51.3	TTTCACACAGGCGCATTCAGGACAAAGTGA	GGTCTTTCTGCTATGCGGCGCTTGACAGC	572
QY	55.9	TGGAAGCGCGGGGAGCGACCCCTGACCGAG	CATGCGAGTGTCCCGAGCTGCAAGTTC	618
Db	57.3	TGGAAGCGCGGGGAGCGACCCCTGACCGAG	CATGCGAGTGTCCCGAGCTGCAAGTTC	632
QY	61.9	CTGCTCCGGCTCAAAAGAGAGACTTTGTGCA	CAGTGTGAGAGACTCATCTCCAGCTG	678
Db	63.3	CTGCTCCGGCTCAAAAGAGAGACTTTGTGCA	CAGTGTGAGAGACTCATCTCCAGCTG	692
QY	67.9	CTGGGCTCTCGGAGCCCGTGAGAAAGAAC	CGGAAGACGACGCCCTGTGCGCCCTCCGTC	738
Db	69.3	CTGGGCTCTCGGAGCCCGTGAGAAAGAAC	CGGAAGACGACGCCCTGTGCGCCCTCCGTC	752
QY	73.9	CTTGCCCTCTGAGGTACCCCTGAGCTGCCCA	CAACCCAGAGAGAGGTCCAGTCTGAAATGCC	798
Db	75.3	CTTGCCCTCTGAGGTACCCCTGAGCTGCCCA	CAACCCAGAGAGAGGTCCAGTCTGAAATGCC	812
QY	79.9	CAGAGCCAGAGACCCAGGAGTGTGAGAGCG	CAGCTCGCGGCTGACAGAGAGAGAGCG	858
Db	81.3	CAGAGCCAGAGACCCAGGAGTGTGAGAGCG	CAGCTCGCGGCTGACAGAGAGAGAGCG	872
QY	85.9	TGCAAGTGTGCTGAGACCGCGCGCTGTGCAT	TCGTCTTTGTGCGCGGCCACCTGTGTC	918
Db	87.3	TGCAAGTGTGCTGAGACCGCGCGCTGTGCAT	TCGTCTTTGTGCGCGGCCACCTGTGTC	932
QY	91.9	TGTGCTGAGTGTGCCCGCGGCTGACAGCTGT	GCCCATCTGAGAGACCCCGCTCCGACGC	978
Db	93.3	TGTGCTGAGTGTGCCCGCGGCTGACAGCTGT	GCCCATCTGAGAGACCCCGCTCCGACGC	992
QY	97.9	CGCGTGCAGACTTCTGTCCTTAGGCGCAGT	GTGCCATGAGCCGCGGACGAGTGGGCTGCAGAGT	1038
Db	99.3	CGCGTGCAGACTTCTGTCCTTAGGCGCAGT	GTGCCATGAGCCGCGGACGAGTGGGCTGCAGAGT	1052
QY	103.9	GCGGCTCCCTGCGCCCTCTGCGCTGTTCGAC	ATGTGTCATGAGTGTGAGGCGTGTGAGATGCGAG	1098
Db	105.3	GCGGCTCCCTGCGCCCTCTGCGCTGTTCGAC	ATGTGTCATGAGTGTGAGGCGTGTGAGATGCGAG	1112
QY	109.9	AGCTGTGTCCATTCAGACACTGACCGCTGAT	TCCCGACCAACCGCCAGGCTGAGAGA	1158
Db	111.3	AGCTGTGTCCATTCAGACACTGACCGCTGAT	TCCCGACCAACCGCCAGGCTGAGAGA	1172
QY	115.9	AGAGAGCCCTTGCTTGTGCGTGGGAGATAG	CTTAACTGTAACCTGTGAGTGTCTTGAAT	1218
Db	117.3	AGAGAGCCCTTGCTTGTGCGTGGGAGATAG	CTTAACTGTAACCTGTGTGAATCTTCTGAAT	1232
QY	121.9	AGAAATTAAGTGGGTTTTCTCTCGAAGGT	1246	
Db	123.3	AGAAATTAAGTGGGTTTTCTCTCGAAGGT	1260	

```

/ APPLICANT: The Scripps Research Institute
/ TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
/ TITLE OF INVENTION: METHODS OF USE THEREOF
/ FILE REFERENCE: T5R1-874.1
/ CURRENT APPLICATION NUMBER: US/10/807,897
/ CURRENT FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/457,009
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 28
/ LENGTH: 1268
/ TYPE: DNA
/ ORGANISM: homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (174)...(1016)
US-10-807-897-28

```

```
Query Match          98.6%; Score 1228; DB 8; Length 1268;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY	19	GGAGAGGCTGTGCTTATCCCTGCTGTCCCAAGGTGAGGCCCGGAGGTCTAGAGCTCCAG	78
Db	33	GGAGAGGCTGTGCTTATCCCTGCTGTCCCAAGGTGAGGCCCGGAGGTCTAGAGCTCCAG	92
QY	79	AAGGGCAGCTGGAGCATATTCTGAGATTGGCATAGGCCCATTTCTGCTGCACAACTG	138
Db	93	AAGGGCAGCTGGAGCATATTCTGAGATTGGCATAGGCCCATTTCTGCTGCACAACTG	152
QY	139	GTCAGAGCCAGTGTTCCTTCACATGGGACCTTAAAGA CAGTGCAGATGCTGCACACGTGGA	198
Db	153	GTCAGAGCCAGTGTTCCTTCACATGGGACCTTAAAGA CAGTGCAGATGCTGCACACGTGGA	212
QY	199	CCACAGCCGAGCACA CTGGGAGAGCGGGTATGTGCCACAGAGAGCGCTGTGACACCCGCG	258
Db	213	CCACAGCCGAGCACA CTGGGAGAGCGGGTATGTGCCACAGAGAGCGCTGTGACACCCGCG	272
QY	259	TCTCTGGGAGCGCTGTCTCTAGCGCTTGACACCTTGACAGAGCTGTAGGACACGTGGATGGG	318
Db	273	TCTCTGGGAGCGCTGTCTCTAGCGCTTGACACCTTGACAGAGCTGTAGGACACGTGGATGGG	332
QY	319	CAGATCTGGGAGCACTCTGCGGCCCTCTGACAGAGAGAAAGAGAGAGGCGCGCGGGCC	378
Db	333	CAGATCTGGGAGCACTCTGCGGCCCTCTGACAGAGAGAAAGAGAGAGGCGCGCGGGCC	392
QY	379	ACCTTGTCCAGGGGGGCTGCTTCCCGCGACATGGAGCTCTAGAGAGTGGCTGTGCTTCC	438
Db	393	ACCTTGTCCAGGGGGGCTGCTTCCCGCGACATGGAGCTCTAGAGAGTGGCTGTGCTTCC	452
QY	439	TTCTATGACTGGCGGCTGACTGTGAGGTGCACCCGAGCTGTGCTGCTGCAGCTTC	498
Db	453	TTCTATGACTGGCGGCTGACTGTGAGGTGCACCCGAGCTGTGCTGCTGCAGCTTC	512
QY	499	TTCCACACAGGCCATCTAGACCAAGGTAGGTGCTTCTTGCTATATGGGGGCTTGCAGAGC	558
Db	513	TTCCACACAGGCCATCTAGACCAAGGTAGGTGCTTCTTGCTATATGGGGGCTTGCAGAGC	572
QY	559	TGGAAGCGCGGGGACGACCCCTTGACGAGACATGCCAAGTGTTCCTCCAGCTGTCACTTC	618
Db	573	TGGAAGCGCGGGGACGACCCCTTGACGAGACATGCCAAGTGTTCCTCCAGCTGTCACTTC	632
QY	619	CTGCTCCGGTCAAAAAGAAAGAGACTTTGCTCCACATGTGTGAGAGACTACTCTCCAGCTTG	678
Db	633	CTGCTCCGGTCAAAAAGAAAGAGACTTTGCTCCACATGTGTGAGAGACTACTCTCCAGCTTG	692
QY	679	CTGGGCTCTTGAGAACCGGTGGAGAAACGGAGAGCGACGCCCTGTGGCGCCCTCCGCTC	738
Db	693	CTGGGCTCTTGAGAACCGGTGGAGAAACGGAGAGCGACGCCCTGTGGCGCCCTCCGCTC	752
QY	739	CTGGCCTCTGGGATCCCTGAGCTGCCACACCCAGAGAGAGATCCAGTCTGAAAGTGC	798

Db 753 CTTGCTCTGGGTAACCTTGAAGTCCACACCCAGAGAGAGTCCATCTGAAAGTCC 812
Qy 799 CAGAGCCAGAGACCCAGGAGATGTGAGCGCAGCTGCGCGGCTTGACAGAGAGAGACG 858
Db 813 CAGAGCCAGAGACCCAGGAGATGTGAGCGCAGCTGCGCGGCTTGACAGAGAGAGACG 872
Qy 859 TGCAGAGTGTGCTGAGACCGCGCGCTTCCATCTGCTTTGTGCGGCTGACCTGATC 918
Db 873 TGCAGAGTGTGCTGAGACCGCGCGCTTCCATCTGCTTTGTGCGGCTGACCTGATC 932
Qy 919 TGTGCTGAGTGTGCGCGCGCTGAGCTGTGCGCCATCTGACAGAGCCCGCTGCGCAGC 978
Db 933 TGTGCTGAGTGTGCGCGCGCTGAGCTGTGCGCCATCTGACAGAGCCCGCTGCGCAGC 992
Qy 979 GCGGTGCGCACCTTCTCTGTCTTGAAGCCAGTGGCCAGTGGCCGAGTGGCTGAGAGT 1038
Db 993 GCGGTGCGCACCTTCTCTGTCTTGAAGCCAGTGGCCAGTGGCCGAGTGGCTGAGAGT 1052
Qy 1039 GGGCTCCCTGCGCCCTCTGCTGTCTTGAAGCTGTGAGTGGCTGAGAGTGGAG 1098
Db 1053 GGGCTCCCTGCGCCCTCTGCTGTCTTGAAGCTGTGAGTGGCTGAGAGTGGAG 1112
Qy 1099 AGCTGTGTCCATCCAGCACTGACAGCCCTGATCCCGACCAACCGCCAGGAGTGA 1158
Db 1113 AGCTGTGTCCATCCAGCACTGACAGCCCTGATCCCGACCAACCGCCAGGAGTGA 1172
Qy 1159 AGAGAGCCCTTGTGCGCGGAGAGTGGCTTAACTGTAAGTGTGAGTCTTCTGAAT 1218
Db 1173 AGGAGCCCTTGTGCGCGGAGAGTGGCTTAACTGTAAGTGTGAGTCTTCTGAAT 1232
Qy 1219 AGAATAAAGTGGGTTTCCCTGGAGGT 1246
Db 1233 AGAATAAAGTGGGTTTCCCTGGAGGT 1260

RESULT 3

US-10-244-586-1

Sequence 1, Application US/10244586
Publication No. US20030087319A1
GENERAL INFORMATION:
APPLICANT: GOMES, BRUCE C.
APPLICANT: KASOF, GARRETT M.
APPLICANT: PROSSER, JUDITH C.
TITLE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: DUB/009901/0270799
CURRENT APPLICATION NUMBER: US/10/244,586
PRIOR APPLICATION NUMBER: US/09/594,119
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1376
TYPE: DNA
ORGANISM: Homo sapiens
US-10-244-586-1

Query Match 98.6%; Score 1228; DB 5; Length 1376;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGCAGGCTGTGCTTATCTCTGCTGTCCAGGGTGGGCGCGGGGCTCAGAGCTCCAG 78
Db 70 GGCAGGCTGTGCTTATCTCTGCTGTCCAGGGTGGGCGCGGGGCTCAGAGCTCCAG 129
Qy 79 AAGGCGCAGTGGGATTTCTGAGTGGCATCAGCCCATTTCTGCTGCAAACTG 138
Db 130 AAGGCGCAGTGGGATTTCTGAGTGGCATCAGCCCATTTCTGCTGCAAACTG 189
Qy 139 GTCAGAGCAGTGTCTCTCCATGAGCACTAAAGACAGTGGCAAGTGGCTGACCGTGA 198

Db 190 GTCAGAGCAGTGTCTCTCCATGAGCACTAAAGACAGTGGCAAGTGGCTGACCGTGA 249
Qy 199 CCAAGCCGAGCCACTGGGAGCGCGTGAAGTCCACGAGAGCCCTGTGACCCCGC 258
Db 250 CCAAGCCGAGCCACTGGGAGCGCGTGAAGTCCACGAGAGCCCTGTGACCCCGC 309
Qy 259 TCTTGGGAGCCCTGTCTTGAAGTCTGGAACACTGACAGAGCTGGAGCACTGTGATGG 318
Db 310 TCTTGGGAGCCCTGTCTTGAAGTCTGGAACACTGACAGAGCTGGAGCACTGTGATGG 369
Qy 319 CAGATCTGGGAGCCAGTGGCGGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
Db 370 CAGATCTGGGAGCCAGTGGCGGCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 429
Qy 379 ACCTTGTCAAGGGGCGCTGCTTCCCGGAGTGGGCTGTGAGAGTTCGCTTGGCCCTTC 438
Db 430 ACCTTGTCAAGGGGCGCTGCTTCCCGGAGTGGGCTGTGAGAGTTCGCTTGGCCCTTC 489
Qy 439 TTTATATAGTGGCGCTGACTGCTGAGTGGCCACCGAGCTGCTGCTGCTGCTGCTTC 498
Db 490 TTTATATAGTGGCGCTGACTGCTGAGTGGCCACCGAGCTGCTGCTGCTGCTGCTTC 549
Qy 499 TTCCACACAGGCCATCAGAGCAAGTGAAGTGGCTTCTGCTATGAGGGGCTTGACAGC 558
Db 550 TTCCACACAGGCCATCAGAGCAAGTGAAGTGGCTTCTGCTATGAGGGGCTTGACAGC 609
Qy 559 TGAAGCGCGGGAGCAGACCCCTGAGACGAGCATGCCAAGTGTTCCTCCAGCTGTCAATT 618
Db 610 TGAAGCGCGGGAGCAGACCCCTGAGACGAGCATGCCAAGTGTTCCTCCAGCTGTCAATT 669
Qy 619 CTGCTCCGCTCAAAAGAGAAAGACTTGTTCACAGTGTGACAGAGACTCATCCAGCTG 678
Db 670 CTGCTCCGCTCAAAAGAGAAAGACTTGTTCACAGTGTGACAGAGACTCATCCAGCTG 729
Qy 679 CTGAGCTCTGAGGACCGCTGAGAGAAACCGAAGACGACCCCTGTGAGCCCTCCGCTC 738
Db 730 CTGAGCTCTGAGGACCGCTGAGAGAAACCGAAGACGACCCCTGTGAGCCCTCCGCTC 789
Qy 739 CTGCTCTGAGGATACCTTGAAGCTGCCCCACACCCAGAGAGAGTCCAGTGTGAAGTGC 798
Db 790 CTGCTCTGAGGATACCTTGAAGCTGCCCCACACCCAGAGAGAGTCCAGTGTGAAGTGC 849
Qy 799 CAGAGCCAGAGACCCAGAGATGTGAGAGCCAGCTGGCGGCTGACAGAGAGAGAGAGC 858
Db 850 CAGAGCCAGAGACCCAGAGATGTGAGAGCCAGCTGGCGGCTGACAGAGAGAGAGAGC 909
Qy 859 TGCAGAGTGTGCTGAGACCGCGCGGTGCTCATGCTTTGTGCGGCTGCGCACCTGGTC 918
Db 910 TGCAGAGTGTGCTGAGACCGCGCGGTGCTCATGCTTTGTGCGGCTGCGCACCTGGTC 969
Qy 919 TGTGCTGAGTGTGCGCGCGCTGACAGCTGTGCCCCATCTGACAGAGCCCGCTCCGAGC 978
Db 970 TGTGCTGAGTGTGCGCGCGCTGACAGCTGTGCCCCATCTGACAGAGCCCGCTCCGAGC 1029
Qy 979 GCGGTGCGCACCTTCTGCTGTCTTGAAGCCAGTGGCCATGAGGCTGGAGTGGCTGAGAGT 1038
Db 1030 GCGGTGCGCACCTTCTGCTGTCTTGAAGCCAGTGGCCATGAGGCTGGAGTGGCTGAGAGT 1089
Qy 1039 GGGCTCCCTGCGCCCTCTGCTGTCTTGAAGCTGTGAGGCTGTGAGGCTGTGAGAGTGGCAG 1098
Db 1090 GGGCTCCCTGCGCCCTCTGCTGTCTTGAAGCTGTGAGGCTGTGAGGCTGTGAGAGTGGCAG 1149
Qy 1099 AGCTGTGTCTCATTCAGACTGACAGCCCTGATTCCTCCGACCAACCGCCAGGAGTGA 1158
Db 1150 AGCTGTGTCTCATTCAGACTGACAGCCCTGATTCCTCCGACCAACCGCCAGGAGTGA 1209
Qy 1159 AAGAGCCCTTGTGCTGGCGTGGGGAGTGGCTTAACTGTAAGTGTGAGTCTTCTGAAT 1218
Db 1210 AAGAGCCCTTGTGCTGGCGTGGGGAGTGGCTTAACTGTAAGTGTGAGTCTTCTGAAT 1269
Qy 1219 AGAATAAAGTGGGTTTCCCTGGAGGT 1246
Db 1270 AGAATAAAGTGGGTTTCCCTGGAGGT 1297

```
RESULT 4
US-10-244-586-2
/ Sequence 2, Application US/10244586
/ Publication No. US20030087319A1
/ GENERAL INFORMATION:
/ APPLICANT: GOMES, BRUCE C.
/ APPLICANT: KASOF, CARRETT M.
/ APPLICANT: PROSSER, JUDITH C.
/ TITLE OF INVENTION: NOVEL PROTEIN
/ FILE REFERENCE: DJB/009901/0270799
/ CURRENT APPLICATION NUMBER: US/10/244,586
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US/09/594,119
/ PRIOR FILING DATE: 2000-06-14
/ PRIOR APPLICATION NUMBER: 60/139,291
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 843
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-244-586-2
```

```
Query Match      67.7%; Score 843; DB 5; Length 843;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 160 ATGGAGCTTAAGACAGTGGCCAGTGGCTGACCCGTGGACACAGCCGAGCCACTGGGCA 219
DB 1 ATGGAGCTTAAGACAGTGGCCAGTGGCTGACCCGTGGACACAGCCGAGCCACTGGGCA 60
QY 220 GCCGCTGATGCTCCACGACGAGAGCGCTGGACCCCGCTCTTGGGCGACCTTGCTCTA 279
DB 61 GCCGCTGATGCTCCACGACGAGAGCGCTGGACCCCGCTCTTGGGCGACCTTGCTCTA 120
QY 280 GGCCCTGACACCTGACAGCTGGGACCACTGATGGGCAATCTGGGCGACCTGGCG 339
DB 121 GGCCCTGACACCTGACAGCTGGGACCACTGATGGGCAATCTGGGCGACCTGGCG 180
QY 340 CCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
DB 181 CCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 400 TTCCCGGCAATGGGCTTGAAGATTGGCTTGGCCCTCTTCTATGACTGGCCGCTGACT 459
DB 241 TTCCCGGCAATGGGCTTGAAGATTGGCTTGGCCCTCTTCTATGACTGGCCGCTGACT 300
QY 460 GCTGAGGTGACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
DB 301 GCTGAGGTGACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 520 AAGGTAGTGTCTTCTTGTCTATGGGGGCTGACAGCTGGAGCGGGGAGAGAGAGAG 579
DB 361 AAGGTAGTGTCTTCTTGTCTATGGGGGCTGACAGCTGGAGCGGGGAGAGAGAGAG 420
QY 580 TGGACGAGCATGCTCAAGTGTTCCTCCAGCTGACAGTTCCTGCTCCGCTCAAAAAGAA 639
DB 421 TGGACGAGCATGCTCAAGTGTTCCTCCAGCTGACAGTTCCTGCTCCGCTCAAAAAGAA 480
QY 640 GACTTGTGTCAAGTGTGACAGAGACTACTCCAGCTGCTGGGCTCTGGAGAGAGAG 699
DB 481 GACTTGTGTCAAGTGTGACAGAGACTACTCCAGCTGCTGGGCTCTGGAGAGAGAG 540
QY 700 GAAGAAGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
DB 541 GAAGAAGCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 760 CTGCCCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
DB 601 CTGCCCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 660
```

```
QY 820 GTGAGAGCCGACAGCTGCGGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
DB 661 GTGAGAGCCGACAGCTGCGGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 880 GCCGTGTCATGCTCTTTGTGTGCGCGGACCACTGATCTGTGCTGAGTGTGCCCCG 939
DB 721 GCCGTGTCATGCTCTTTGTGTGCGCGGACCACTGATCTGTGCTGAGTGTGCCCCG 780
QY 940 CTGACAGCTGTGCCCCATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
DB 781 CTGACAGCTGTGCCCCATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 1000 TAG 1002
DB 841 TAG 843
```

```
RESULT 5
US-10-807-897-26
/ Sequence 26, Application US/10807897
/ Publication No. US20040192631A1
/ GENERAL INFORMATION:
/ APPLICANT: Xiang, Kong
/ APPLICANT: Zhou, He
/ APPLICANT: Reisfeld, Ralph A.
/ APPLICANT: The Scripps Research Institute
/ TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
/ FILE REFERENCE: TSI-874.1
/ CURRENT APPLICATION NUMBER: US/10/807,897
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/457,009
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 26
/ LENGTH: 1322
/ TYPE: DNA
/ ORGANISM: homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (174)...(1070)
US-10-807-897-26
```

```
Query Match      63.6%; Score 793; DB 8; Length 1322;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 19 GGAGAGCCCTGACCTATCCCTGCTGTCCCAAGGTGGGCCCCGGGGTCAAGAGCTTCAG 78
DB 33 GGAGAGCCCTGACCTATCCCTGCTGTGTCCCAAGGTGGGCCCCGGGGTCAAGAGCTTCAG 92
QY 79 AAGGGCCAGCTGGGCAATTTGAGATTGGCATCAGCCCCCATTTGCTGCAAAACTTG 138
DB 93 AAGGGCCAGCTGGGCAATTTGAGATTGGCATCAGCCCCCATTTGCTGCAAAACTTG 152
QY 139 GTCAAGGACAGTTCCTCCATATGGAGACTTAAGACAGTGTCCAGTGTGCAACCTG 198
DB 153 GTCAAGGACAGTTCCTCCATATGGAGACTTAAGACAGTGTCCAGTGTGCAACCTG 212
QY 199 CCACAGCCGAGCACTGGGAGAGCGGTATGTCCACGAGAGAGAGAGAGAGAGAGAG 258
DB 213 CCACAGCCGAGCACTGGGAGAGCGGTATGTCCACGAGAGAGAGAGAGAGAGAGAG 272
QY 259 TCTCTGGGAGAGCCCTGTCTTAAAGCTTGAACCTTGACAGAGCTTGGAATGGG 318
DB 273 TCTCTGGGAGAGCCCTGTCTTAAAGCTTGAACCTTGGAATGGGAGATGGG 332
QY 319 CAGATCTGTGGCCAGCTGCGGCGCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 333 CAGATCTGTGGCCAGCTGCGGCGCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAG 392
```



```
; Sequence 12, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 12
; LENGTH: 1168
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(897)
US-10-188-646-12

Query Match          48.2%; Score 601; DB 6; Length 1168;
Best Local Similarity 99.8%; Pred. No. 1.9e-294;
Matches 651; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 160 ATGGGACCTTAAGACAGTGCAGTGCCTGACCTGTGACACACAGCCGACCTGTGGCA 219
DB 1 ATGGGACCTTAAGACAGTGCAGTGCCTGACCTGTGACACACAGCCGACCTGTGGCA 60
QY 220 GCCGGTATGTGTCCACGACGAGCGCTGTGACCCCGCTCTGTGGGAGCCCTGTCTTA 279
DB 61 GCCGGTATGTGTCCACGACGAGCGCTGTGACCCCGCTCTGTGGGAGCCCTGTCTTA 120
QY 280 GGCTTGACACCTTGACAGCTGTGGACCACTGTATGGGACAGATCTGGGCTGAGTGG 339
DB 121 GGCTTGACACCTTGACAGCTGTGGACCACTGTATGGGACAGATCTGGGCTGAGTGG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 400 TTCCCGGCAATGGGCTGTGAGAGTGTGCTGTGGCTCTTCTATGACTGTGCGCTGACT 459
DB 241 TTCCCGGCAATGGGCTGTGAGAGTGTGCTGTGGCTCTTCTATGACTGTGCGCTGACT 300
QY 460 GCTGAGGTGCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 519
DB 301 GCTGAGGTGCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 360
QY 520 AAGGTGAGTGTCTTCTTCTATGAGGAGGCTGTGACAGCTGTGAAAGCGGGGAGAGACCC 579
DB 361 AAGGTGAGTGTCTTCTTCTATGAGGAGGCTGTGACAGCTGTGAAAGCGGGGAGAGACCC 420
QY 580 TGAACGAGATGCAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 639
DB 421 TGAACGAGATGCAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 480
QY 640 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTGTGGAGCCGCTGG 699
DB 481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTGTGGAGCCGCTGG 540
QY 700 GAAGAAACCGGAAGACGAGCGCCCTGTGGCCCGCTGTGGCTGTGGCTGTGGCTGTGG 759
DB 541 GAAGAAACCGGAAGACGAGCGCCCTGTGGCCCGCTGTGGCTGTGGCTGTGGCTGTGG 600
QY 760 CTGGCCACACCCAGAGAGAGAGTGTCACTGTAAGAGTGTGCGGAGAGCCAGAGAG 811
DB 601 CTGGCCACACCCAGAGAGAGAGTGTCACTGTAAGAGTGTGCGGAGAGCCAGAGAG 652

RESULT 10
US-10-203-708-21
; Sequence 21, Application US/10203708
; Publication No. US20030149238A1
```

```
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.I.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/10/203,708
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-708-21

Query Match          42.7%; Score 532; DB 6; Length 1068;
Best Local Similarity 100.0%; Pred. No. 2.1e-259;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 ATGGGACCTTAAGACAGTGCAGTGCCTGTGACCTGTGACACACAGCCGACCTGTGGCA 219
DB 1 ATGGGACCTTAAGACAGTGCAGTGCCTGTGACCTGTGACACACAGCCGACCTGTGGCA 60
QY 220 GCCGGTATGTGTCCACGACGAGCGCTGTGACCCCGCTCTGTGGGAGCCCTGTCTTA 279
DB 61 GCCGGTATGTGTCCACGACGAGCGCTGTGACCCCGCTCTGTGGGAGCCCTGTCTTA 120
QY 280 GGCTTGACACCTTGACAGCTGTGGACCACTGTATGGGACAGATCTGGGCTGAGTGG 339
DB 121 GGCTTGACACCTTGACAGCTGTGGACCACTGTATGGGACAGATCTGGGCTGAGTGG 180
QY 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 400 TTCCCGGCAATGGGCTGTGAGAGTGTGCTGTGGCTCTTCTATGACTGTGCGCTGACT 459
DB 241 TTCCCGGCAATGGGCTGTGAGAGTGTGCTGTGGCTCTTCTATGACTGTGCGCTGACT 300
QY 460 GCTGAGGTGCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 519
DB 301 GCTGAGGTGCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 360
QY 520 AAGGTGAGTGTCTTCTTCTATGAGGAGGCTGTGACAGCTGTGAAAGCGGGGAGAGACCC 579
DB 361 AAGGTGAGTGTCTTCTTCTATGAGGAGGCTGTGACAGCTGTGAAAGCGGGGAGAGACCC 420
QY 580 TGAACGAGATGCAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 639
DB 421 TGAACGAGATGCAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 480
QY 640 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTGTGGAGCCGCTGG 691
DB 481 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGCTGTGGAGCCGCTGG 532

RESULT 11
US-10-188-646-11
; Sequence 11, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
```


Oy 503 ACACAG 508
Db 2543 ACACAG 2548

Search completed: April 22, 2006, 10:02:38
Job time : 987 secs

Db	12	GGCTGGACACCTGACAGAGCTTGGACCAAGTGGATGGCAGACTCTGGCCAGCTGGG	187
Qy	340	CCCTTGACAGAGGAGGAAAGGAGAGGAGCGCCGGGGCCACTTGTCCAGGGGGCTGGCC	395
Db	181	CCCTTGACAGAGGAGGAAAGGAGAGGAGCGCCGGGGCCACTTGTCCAGGGGGCTGGCC	240
Qy	400	TTCCCGGCAATGGGGCTCTAGAGAGTTGGCTCTGGCTCCTTCTATGACTGGCCGCTGACT	459
Db	241	TTCCCGGCAATGGGGCTCTAGAGAGTTGGCTCTGGCTCCTTCTATGACTGGCCGCTGACT	300
Qy	460	GCTGAGGTGCACCCGAGCTGAGCTGTGCGCGCTTCTTCCACAGAGGCATCAGAGAC	519
Db	301	GCTGAGGTGCACCCGAGCTGAGCTGTGCGCGCTTCTTCCACAGAGGCATCAGAGAC	360
Qy	520	AAAGTGAAGTGTCTTCTTCTGCTATGAGGGGCTGCAGAGCTGAGAAAGCGGGGAGACCCC	579
Db	361	AAAGTGAAGTGTCTTCTTCTGCTATGAGGGGCTGCAGAGCTGAGAAAGCGGGGAGACCCC	420
Qy	580	TGACGAGAGATCCCAAGTGTCTCCCAAGCTGTCACTTCTGTCTCCGATCAAAAAGAGA	639
Db	421	TGACGAGAGATCCCAAGTGTCTCCCAAGCTGTCACTTCTGTCTCCGATCAAAAAGAGA	480
Qy	640	GACTTTGTCCACAGTGTGCAGAGAGCTCACTCCGAGCTCGGGGCTCTGGG	691
Db	481	GACTTTGTCCACAGTGTGCAGAGAGCTCACTCCGAGCTCGGGGCTCTGGG	532

```

RESULT: 2
US-11-135-855-22
Sequence 22, Application US/11135855
Publication No. US20050255557A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.L.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPS0013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: 10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 769
TYPE: DNA
ORGANISM: Homo sapiens
US-11-135-855-22

```

Query Match	35.9%	Score 447;	DB 14;	Length 769;
Best Local Similarity	100.0%	Pred. No. 6.3e-212;		
Matches 447; Conservative	0;	Mismatches	0;	Gaps 0;

OY	160	ATGGACCTTAAAGCAAGTCGCAAGTCCCTGCACCTGTGACACACACCGGAGCACTGGCA	219
Db	1	ATGGACCTTAAAGCAAGTCGCAAGTCCCTGCACCGTGAACACACCGAGCACTGGGCA	60
OY	220	GCCGGTGAATGATCCACGCGAGGAGGCGTGTGACCCCGCTCTCTGGGGACGCCCCGTCTTA	279
Db	61	GCCGGTGAATGATCCACGCGAGGAGGCGTGTGACCCCGCTCTCTGGGGAGCCCCGTCTTA	120
OY	280	GGCGTGGACACCTTGGGAGACCTTGGGACCACTGTGATGGGACAGATCCTGGGCGACGTGCG	339
Db	121	GGCGTGGACACCTTGGGAGACCTTGGGACCACTGTGATGGGACAGATCCTGGGCGACGTGCG	180
OY	340	CCCCTGACAGAGAGAGAGAGAGAGAGAGGCGCCGGGGCGACCTTGTCAAGGGGGCCTTGCC	399
Db	181	CCCCTGACAGAGAGAGAGAGAGAGAGAGGCGCCGGGGCGACCTTGTGTCAAGGGGGCCTTGCC	240

QY 400 TTCCCGGACATGGAGCTCTAGAGAGTTGCGCTCGGGCTCTTCTTATATGACTGCGCGTGA CT 459

Db 241 TTCCCGGACATGGAGCTCTAGAGAGTTGCGCTCGGGCTCTTCTTATATGACTGCGCGTGA CT 300

QY 460 GCTGAGGTGCACCCGAGCTGCTGCTGCCTGCCTGCTTCTTCCACACAGGCGCATCAGGAC 519

Db 301 GCTGAGGTGCACCCGAGCTGCTGCTGCCTGCCTGCTTCTTCCACACAGGCGCATCAGGAC 360

QY 520 AAGGTAGGTGCTTCTTCTGCTATATGGGGGCTGACAGCTGGAAGCGCGGAGCGACCCC 579

Db 361 AAGGTAGGTGCTTCTTCTGCTATATGGGGGCTGACAGCTGGAAGCGCGGAGCGACCCC 420

QY 580 TGGACGAGCATGCCAAGGTGTTCCCC 606

Db 421 TGGACGAGCATGCCAAGGTGTTCCCC 447

```

RESULT 3
US-10-310-914A-81037/C
; Sequence 81037, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Yvruze
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 06087.0200.CF0501
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 81037
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-81037

```

Query Match	2.2%	Score 28	DB 8	Length 28
Best Local Similarity	100.0%	Pred. No.	0.0027	
Matches	28	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
Qy	1177	GTGGGGATGGCTTAACGTACCTCGTTT	1204	
Db	28	GTGGGGATGGCTTAACGTACCTCGTTT	1	

```

RESULT 4
US-10-310-914A-81063/c
; Sequence 81063, Application US/10310914A
; Publication No. US20060003222A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuznet
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81063
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-81063

```

```

Query Match      2.1%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      45 CCCCAAGGCTAGGCCCCCGGAGGCTCAGG 70
|||||

```

Db 26 CCCAGGTGGCCCCGGGGTTCAGG 1

RESULT 5

US-10-310-914A-81062/c
; Sequence 81062, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200, chusoi
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81062
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-81062

Query Match 2.0%; Score 25; DB 8; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.085; Mismatches 0; Indels 0; Gaps 0;

Qy 46 CCCAGGTGGCCCCGGGGTTCAGG 70
Db 25 CCCAGGTGGCCCCGGGGTTCAGG 1

RESULT 6

US-11-121-849-61904
; Sequence 61904, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61904
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61904

Query Match 2.0%; Score 25; DB 14; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.085; Mismatches 0; Indels 0; Gaps 0;

Qy 1020 GCCAGGTGGCTGCAGAGTGGGCTC 1044
Db 1 GCCAGGTGGCTGCAGAGTGGGCTC 25

RESULT 7

US-11-121-849-61905
; Sequence 61905, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03

; PRIOR APPLICATION NUMBER: 60/567,949

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 61905

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien
US-11-121-849-61905

Query Match 2.0%; Score 25; DB 14; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.085; Mismatches 0; Indels 0; Gaps 0;

Qy 1056 CTGCTGTTCGACGTGTCTG 1080
Db 1 CTGCTGTTCGACGTGTCTG 25

RESULT 8

US-11-121-849-61906
; Sequence 61906, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61906
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61906

Query Match 2.0%; Score 25; DB 14; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.085; Mismatches 0; Indels 0; Gaps 0;

Qy 1060 CTGTTCTGACGTGTCTG 1084
Db 1 CTGTTCTGACGTGTCTG 25

RESULT 9

US-11-121-849-61907
; Sequence 61907, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61907
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61907

Query Match 2.0%; Score 25; DB 14; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.085; Mismatches 0; Indels 0; Gaps 0;

```
QY      1110 ATCCAGACTGACGACCCCTGATTC 1134
      |||
      1 ATCCAGACTGACGACCCCTGATTC 25

RESULT 10
US-11-121-849-61908
; Sequence 61908, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61908
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61908

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1138 GACCACCGCCGAGGTGAGAGAGA 1162
      |||
      1 GACCACCGCCGAGGTGAGAGAGA 25

RESULT 11
US-11-121-849-61909
; Sequence 61909, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61909

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1181 GGGATGGCTTAAGTACTGTTG 1205
      |||
      1 GGGATGGCTTAAGTACTGTTG 25

RESULT 12
US-11-121-849-61910
; Sequence 61910, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61910

; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61910

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1183 GATGGCTTAAGTACTGTTGGA 1207
      |||
      1 GATGGCTTAAGTACTGTTGGA 25

RESULT 13
US-11-121-849-61911
; Sequence 61911, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61911
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61911

Query Match      2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1186 GGCTTAAGTACTGTTGATGC 1210
      |||
      1 GGCTTAAGTACTGTTGATGC 25

RESULT 14
US-11-121-849-61912
; Sequence 61912, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61912
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61912
```

Query Match 2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1190 TAACTGACCTGTTGGATGCTTCT 1214
Db 1 TAACTGACCTGTTGGATGCTTCT 25

RESULT 15

US-11-121-849-61913
; Sequence 61913, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61913

Query Match 2.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1192 ACTGACCTGTTGGATGCTTCTGA 1216
Db 1 ACTGACCTGTTGGATGCTTCTGA 25

Search completed: April 22, 2006, 09:51:10
Job time : 705 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, **using frame plus p2n model**

Run on: April 24, 2006, 09:59:43 ; Search time 4443 Seconds
(without alignments)
3953.326 Million cell updates/sec

Title: US-09-762-577B-12
Perfect score: 309
Sequence: 1 MGPRDSAKCXHRGQPSHWA.....GLQGLPAPLCIFMTVFAC 309

Scoring table: 01000
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word sizes: 1

Total number of hits satisfying chosen parameters: 11757816

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n_model -DEV=xlp
-Q=/abs/ABSSWEB_spool/US09762577/runat_24042006_105921_763/app_query.fasta.1
-DB=GenEmbl -QMT=fastcap -SUFFIX=p2nol1.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NOR=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs06p
-USER=US09762577@CGN_1_1_7415_@runat_24042006_105921_763 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : GenEmbl.*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total of the result being printed, and is derived by analysis of the score distribution.

SUMMARIES			
Result No.	Score	Match Length	ID
1	280	90.6	840 6 BD167853
2	280	90.6	840 6 BD185365
3	280	90.6	843 6 AX067716

Description
BD167853 Survivin-
BD185365 Survivin-
AX067716 Sequence

4	280	90.6	1260	6	CO896991	Sequence
5	280	90.6	1260	6	CS113085	Sequence
6	280	90.6	1260	8	AF311388	Homo sapi
7	280	90.6	1301	8	AV358835	Homo sapi
8	280	90.6	1376	6	AX067715	Sequence
9	218	70.6	672	6	BD167852	Survivin-
10	218	70.6	672	6	BD185364	Survivin-
11	218	70.6	723	6	BD167851	Survivin-
12	218	70.6	723	6	BD185363	Survivin-
13	217	70.2	1168	8	AF301009	Homo sapi
14	217	70.2	1312	6	CO896990	Sequence
15	217	70.2	1312	8	BC014475	Homo sapi
16	217	70.2	1337	6	BD248275	DNA encod
17	217	70.2	1337	6	AR242238	Sequence
18	217	70.2	1370	8	AV358836	Homo sapi
19	210	68.0	1021	8	AY517497	Homo sapi
20	117	37.9	615	6	CQ721033	Sequence
21	117	37.9	4810	8	HS430928	Homo sapi
22	117	37.9	184223	8	HS4261N11	Human DNA
23	68	22.0	204	6	BD167849	Survivin-
24	68	22.0	204	6	BD185361	Survivin-
25	54	17.5	404	6	AX071974	Sequence
26	47	15.2	141	6	BD167850	Survivin-
27	47	15.2	141	6	BD185362	Survivin-
28	44	14.2	226	6	AR379789	Sequence
29	33	10.7	726	10	BV639843	S217P6023
30	30	9.7	200	6	AR269653	Sequence
31	30	9.7	200	6	AR379842	Sequence
32	18	5.8	205927	9	AL954707	Mouse DNA
33	16	5.2	532	10	BV267018	S235P6464
34	16	5.2	103853	14	AC135298	Rattus no
35	16	5.2	264967	14	AC098373	Rattus no
36	14	4.5	362	5	AY326791	Ameletus
37	14	4.5	372	6	CQ676063	Sequence
38	14	4.5	1435	6	BD185748	Human inh
39	14	4.5	1550	4	SSU79142	Sus scrofa
40	14	4.5	1601	6	AR379952	Sequence
41	14	4.5	1770	9	AF183431	Rattus no
42	14	4.5	1904	4	AY267258	Bos tauru
43	14	4.5	1946	5	AF442500	Danio rer
44	14	4.5	2278	5	AY184377	Ictalurus
45	14	4.5	2380	8	BC016174	Homo sapi

ALIGNMENTS

RESULT 1	BD167853	840 bp	DNA	linear	PAT 17-JAN-2003
LOCUS	Survivin-like polypeptide and its DNA.				
DEFINITION	BD167853				
ACCESSION	BD167853.1	GI:27873665			
VERSION	WO 0233071-A/5.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 840)				
AUTHORS	Survivin-like polypeptide and its DNA				
JOURNAL	Patent: WO 0233071-A 5 25-APR-2002;				
COMMENT	TAKEEDA CHEMICAL INDUSTRIES LTD, HIROSHI TANAKA, ISAO KAIEDA				
	OS Homo sapiens (human)				
	PN WO 0233071-A/5				
	PD 25-APR-2002				
	PF 17-OCT-2001 WO 2001JP009071				
	PR 17-OCT-2000 JP 00P 316721, 20-DEC-2000 JP 00P 386809				
	HIROSHI TANAKA, ISAO KAIEDA				
	PC C12N15/09, C12N15/12, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/09, C12N5/12, C07K16/18, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, PC				

A61K31/711,
PC A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00 CC
Survivin-like polypeptide and its DNA
FH Key Location/Qualifiers
FT source 1..840
Location/Qualifiers
FT /organism="Homo sapiens (human)".
source 1..840
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment.Scores:
Pred. No.: 3.5e-272 Length: 840
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x BD167853 (1-840)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 1 ATGGGGCCCTAAAGACAGTGGCCAAAGTGGCTGCACCGTGGACCAAGCCGACCTGGGCA 60

QY 21 AlaGlyAspGlyProThrGlnGlnLysGlyGlyProArgSerLeuGlySerProValLeu 40
Db 61 GCCGGTATAGTGTCCCAAGACAGAGCGGTGTGGACCCCGCTGTGGAGCCCTGTGCTTA 120

QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlnLysGlnLeuArg 60
Db 121 GGCTTGACACCTGCAGACGCTGGAGCACCTGGATGGAGATCTTGGGGCCAGCTGGCG 180

QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 181 CCCCTGCAG 240

QY 81 PheProGlyMetGlySerGlnGlnGlnLysLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
Db 241 TTCCTGGGCGATGGGCTCTGAGAGTGGCTGCTGCTCTCTTCTTATGACTGGCCGCTGACT 300

QY 101 AlaGlnValaProProGlnLysLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 301 GCTGAGGTGCACCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 121 LysValaArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db 361 AAGGTGAGGTGCTTCTTCTGCTATGGGGGCTGCAAGCTGGAGCGCGGGACGACCC 420

QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 421 TGGACCGAGCATGCCAAGTGGTCCCGACGCTGCAAGTCTCTGCTCGGTCGCAAAAGAGA 480

QY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db 481 GACTTTGTCTCAAGTGTGCAGAGACTCCTCCAGCTGGGCTCTCTGGACCCCGTGG 540

QY 181 GlnGlnProGlnAspAlaAlaProValaAlaProSerValaProAlaSerGlyTrpProGln 200
Db 541 GAAGAAACCGGAAGACGACGCCCTGTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY 201 LeuProThrProArgArgGlnValaGlnSerGlnSerAlaGlnGlnProGlnValaArgAsp 220
Db 601 CTGCCACACCCAGAGAGAGAGTCCAGTCAAGTCCAAAGTCCAGAGAGCCAGAGCCAGGAT 660

QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 661 GTGGAGGGCGACCTCGCGGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720

QY 241 AlaValSerTrpLeuValPheValaProCysGlyHisLeuValaCysAlaGlnCysAlaProGly 260
|||||

Db 721 GCCGTGCATGCTTTGTGTGCGCGGCCCACTGCTGTGCTGAGTGTCCCGCC 780

QY 261 LeuGlnLeuCysProIleCysArgAlaProValaArgSerArgValaArgThrPheLeuSer 280
|||||

Db 781 CTGCAAGTGTGCTCCATCTGCAGAGACCCCGTCCGACAGCCCGTGGCGACCTTCTGTGCC 840

RESULT 2
BD185365 840 bp DNA linear PAT 17-JUN-2003
LOCUS
DEFINITION
Survivin-like polypeptide and its DNA.
ACCESSION
BD185365
VERSION
BD185365.1 GI:31877565
KEYWORDS
JP 2002355062-A/5.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 840)
Tanaka,H. and Kaleda,I.
Survivin-like polypeptide and its DNA
Patent: JP 2002355062-A-5 10-DEC-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT
OS Homo sapiens (human)
PN JP 2002355062-A/5
PD 10-DEC-2002
PF 16-OCT-2001 JP 2001318533
PI HIROSHI TANAKA,ISAO KAIEDA
PC C12N15/09,A61K31/7088,A61K38/55,A61K39/395,A61K48/
PC 00 A61P35/00
PC A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19,PC
C12N1/21,
PC C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,PC
G01N33/53,
PC G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64
CC Survivin-like polypeptide and its DNA
FH Key Location/Qualifiers
FT source 1..840
Location/Qualifiers
FT /organism="Homo sapiens (human)".
source 1..840
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment.Scores:
Pred. No.: 3.5e-272 Length: 840
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x BD185365 (1-840)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 1 ATGGGGCCCTAAAGACAGTGGCCAAAGTGGCTGCACCGTGGACCAAGCCGACCTGGGCA 60

QY 21 AlaGlyAspGlyProThrGlnGlnLysGlyGlyProArgSerLeuGlySerProValLeu 40
Db 61 GCCGGTATAGTGTCCCAAGACAGAGCGGTGTGGACCCCGCTGTGGAGCCCTGTGCTTA 120

QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlnLysGlnLeuArg 60
Db 121 GGCTTGACACCTGCAGACGCTGGAGCACCTGGATGGAGATCTTGGGGCCAGCTGGCG 180

QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 181 CCCCTGCAG 240

QY 81 PheProGlyMetGlySerGlnGlnGlnLysLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
|||||

Db	241	TTCCCCGGATGGGCTCTGAGAGTTGGCTCTGGCTCTTCTTAAGACTGGCCCTGA	300
QY	101	AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120
Db	301	GCTGAGGTGCACCCGAGCTGCTGGCTGCTGCCGGCTTCTTCCACAGGCGCATCAGNC	360
QY	121	LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro	140
Db	361	AAAGTGAGGTGCTTCTTCTGCTATAGGGGGCTGCAGAGCTGGAAACGGGGGACACCC	420
QY	141	TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuAspSerLysGlyArg	160
Db	421	TGCAGGAGCAGTCCCAAGTGGTTCCTCCAGCTGCTCAGTTCCTCCGCTCAAAAGAAAG	480
QY	161	AspPheValHisSerValGlnGlnIuThrHisSerGlnLeuGlySerTrpAspProTrp	180
Db	481	GACTTGTTCACAGCTGCAGAGACTCACTCCAGCTGGCTGGCTCTGGACCCGTGG	540
QY	181	GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu	200
Db	541	GAAAGACCGAAGACGACGCCCCCTGTGGCCCCCTCGTCCCTGTGGGTAGACCTTAG	600
QY	201	LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyValaArgAsp	220
Db	601	CTGCCACACCCAGGAGAGAGGTCCAGTCTGAAGTCCACGAGACCCAGAACCGAGAT	660
QY	221	ValGluAlaGlnLeuArgArgLeuGlnGluGluArgThrCysLysValCysLeuAspArg	240
Db	661	GTGGAGGGCGCAGCTCGCGGCTGCAGGAGAGAGACGTGCMAAGTGTGCTGGACCGC	720
QY	241	AlaValSerLeuValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly	260
Db	721	GCGGTGTCATGCTTTGTGCGCGGCGCACCTGTGCTGTGAGATGTGCCCCCGGC	780
QY	261	LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer	280
Db	781	CTGCAGCTGTGCCCATCTGCAGAGACCCCCGTCGCCAGCCGCGTGCACCTTCTGTCC	840
RESULT 3			
AX067716		843 bp	DNA linear PAT 19-JAN-2001
LOCUS	AX067716		
DEFINITION	Sequence 2 from Patent WO0077201.		
LOCATION	AX067716		
ACCESSION	AX067716.1	GI:12329603	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homidae; Homo.		
REFERENCE			
AUTHORS	1		
TITLE	Gomes,B.C., Kasof,G.M. and Prosser,J.C.		
JOURNAL	Living; inhibitor-of-apoptosis protein-3 (iap-3)		
	Patent: WO 0077201-A 2 21-DEC-2000;		
FEATURES			
source	location/Qualifiers		
	1..843		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Alignment Scores:			
Pred. No.:	3,51e-272	Length:	843
Score:	280..00	Matches:	280
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	90.6%	Indels:	0
Db:	6	Gaps:	0

Oy		I	MetGlyProLysAspSerAlaIysCysLeuHiValArgIleProGlnProSerHisTrpAla	20
Db		I	ATGGAGCACTTAAGAACAAGTGCACAAAGCGCTTGACCGGTGAACCAAGCCACAGCATCGGACA	60
Oy		21	AAGIYAAPGILYProThrGlnGluNargCysGlyProArgSerLeuGlySerProValLeu	40
Db		61	GCCGGTAGATTGTCACCACAGAGAGCGCTGTGGAACCCGCCCTCTTGGGACAGCCCTGTCTTA	120
Oy		41	GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyInlIeLeuGlyGlnLeuNarg	60
Db		121	GGCTTGACACTCTGCAGAGCGCTGGGACCAACGTGATGGGAGATCTCTGGCACGCTGGCG	180
Oy		61	ProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	80
Db		181	CCCCCTGACAG	240
Oy		81	PheProGlyMetGlySerGluGluLeuNargLeuNargLeuNargLeuNargLeuNargLeuNarg	100
Db		241	TTCCTCCGCGAATGGGCTCTGAGAGATTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	300
Oy		101	AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120
Db		301	GCTAGAGTGCACCCAGACTGCTGGCTGCTGCCGCTTTCTTCACACAGGCGCATAGGAC	360
Oy		121	LysValAlaGlyCysPhePheCysTyrlGlyGlyLeuGlnSerTrpLysArgIYAASPPro	140
Db		361	AAGGTGAAGTGTCTTCTTCTGCTAATGGGGGCTGTGACAGACTGGAAGCGCGGAGACGACCC	420
Oy		141	TrpThrGlnHisAlaIleValTrpPheProSerCysGlnPheLeuNargSerIleGlyArg	160
Db		421	TGAGAGGAGCATGCCAAGTGTCTCCCAAGCTGTCACTTCGCTCCGGTCAAAGGAAGA	480
Oy		161	AspPheValHisSerValGlnGluIleThriHisSerGlnLeuNargLysSerTrpAspProTrp	180
Db		481	GACTTTGTTCACAGTGTGCAGAGAACACTACCTCCAGCTGCTGGGCTCTGGGAGACCCGTGAC	540
Oy		181	GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTYrProGlu	200
Db		541	GAAGAACCGGAAGACGACGCCCTGTGGCCCCCTCGCTCCGCTCGGGGACCTGAG	600
Oy		201	LeuProThrProAlaGArgGluValAlaGlnSerGlnSerAlaGlnGluProGlyValAlaArgAsp	220
Db		601	CTGCCCAACCCAGAGAGAGAGAGTGCAGTCTAAAGTGCACAGAGCCGAGGACGAGGAT	660
Oy		221	ValGluAlaGlnLeuNargXArgLeuGlnGluGluGluGluGluGluGluGluGluGluGluGluGlu	240
Db		661	GTGAGGCGGCACTGCGCGCGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	720
Oy		241	AlaValSerIleValPheValProCysGlyHisIleValCysAlaGluCysAlaProGly	260
Db		721	GCCGTGTCAATCGTCTTTGTGTCCGAGGGGACCACTGGTGTGTGCTGAGTGTGCCCGGC	780
Oy		261	LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValAlaThrPheLeuSer	280
Db		781	CTGCAGCTGTGCCCATCTGCAGAGAGCCCGCTCCGACGCGCGTGCACCTTCTGTCC	840
RESULT 4				
CQ896991				
LOCUS	CQ896991	1260 bp	DNA	linear PAT 08-NOV-2004
DEFINITION	Sequence 11 from Patent WO2004091388.			
ACCESSION	CQ896991			
VERSION	CQ896991.1 GI:55581833			
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Homnidae; Homo.			
REFERENCE	Butz,K., Cinkovic-Wertens,I. and Hoppe-Seyler,F.			
AUTHORS	LYVIN-SPECIFIC BIRNAS FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS			
TITLE	Patent: WO 2004091388-A 11 28-OCT-2004;			
JOURNAL	Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts			

FEATURES (IDE) Location/Qualifiers
source 1..1260
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 4.88e-272 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 6 Gaps: 0
US-09-762-577B-12 (1-309) x CQ896991 (1-1260)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 174 ATGGGACCTTAAGACAGTGGCCAGTGCCTGCACCGTGGACCAAGCCGAGCCACTGGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGlnuArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGATATGGTCCACGACGAGGAGCGCTGTGACCCCGCTCTCTGGGACGCCCTGTCTTA 293
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 294 GGCTTGAACACCTTCAAGCCTGGAGCACGTGATGGCAGATCCTGGGCCAGCTGCCG 353
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCTGACAGAGGAG 413
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 414 TTCCCCGGCATGGGCTCTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
QY 101 AlaGlyValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGCACCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspPro 140
Db 534 AAGGTAGAGTCTTCTTCTGCTATGGGGGCTGACAGCTGAGAGCGGGAGACACACCC 593
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 594 TGGACGGAGCATCCAAAGTGGTCCCCCACTGTCAAGTCTCTCGGTCAAAAGAGAGA 653
QY 161 AspPheValHisSerValGlnGlnLthrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db 654 GACTTGTGCCACGCTGTGAGAGAGACTCACTCCAGCTGTGGCTCTCGGGACCCGG 713
QY 181 GlnGlnProGlnuAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db 714 GAAAGAACCGAAGACGCAAGCCCTGTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 773
QY 201 LeuProThrProArgArgGlnuAlaGlnSerGlnuSerAlaGlnGlnProGlnValArgAsp 220
Db 774 CTGCCACACCCAGAGAGAGAGTGTCCAGTCTGAAATGTGCCAGAGCCAGAGCCAGGAT 833
QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 834 GTGGAGGCCAGCACTGGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY 241 AlaValSerIleValPheValProCysGlyHisIleuValCysAlaGlnCysAlaProGly 260
Db 894 GCCGATGCATGCTTTGTGTGCGCGGCGGCACTGGTCTTGTCTGAGTGTGCCCCGGC 953
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGACGCTGTGCCCATCTGTGAGAGGCCCGCTCGCAGAGCCGCTGCGCACCTTCTGTCC 1013

RESULT 5
CS113085 1260 bp DNA linear PAT 24-JUN-2005
LOCUS CS113085 Sequence 103 from Patent WO2005054507.
DEFINITION CS113085
ACCESSION CS113085
VERSION CS113085.1 GI:68224657
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE
1 Corfe, B. and Chirakkal, H.
AUTHORS
TITLE Gene screen
JOURNAL Patent: WO 2005054507-A 103 16-JUN-2005;
University of Sheffield (GB)
FEATURES
source Location/Qualifiers
1..1260
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 4.88e-272 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) x CS113085 (1-1260)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 174 ATGGGACCTTAAGACAGTGGCCAGTGCCTGCACCGTGGACCAAGCCGAGCCACTGGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGlnuArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGATATGGTCCACGACGAGGAGCGCTGTGACCCCGCTCTCTGGGACGCCCTGTCTTA 293
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 294 GGCTTGAACACCTTCAAGCCTGGAGCACGTGATGGCAGATCCTGGGCCAGCTGCCG 353
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCTGACAGAGGAG 413
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 414 TTCCCCGGCATGGGCTCTGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
QY 101 AlaGlyValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGCACCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspPro 140
Db 534 AAGGTAGAGTCTTCTTCTGCTATGGGGGCTGCGAGACTGGAACCGGGGACCAACCC 593
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 594 TGGACGGAGCATCCAAAGTGGTCCCCCACTGTCAAGTCTCTCGGTCAAAAGAGAGA 653
QY 161 AspPheValHisSerValGlnGlnLthrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db 654 GACTTGTGCCACGCTGTGAGAGAGACTCACTCCAGCTGTGGCTCTCGGGACCCGG 713
QY 181 GlnGlnProGlnuAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200

Db	714	GAGGAACCGGAAAGCAGCACCCCTGTGGCCCCCTCGTGCCTTGCTGGGNAACCTGAG	773
OY	201	LeuPcOTHrPrOArXArgGLuValGlnSerGIuSerAlaGlnGluProGlyAlaAraGsp	220
Dd	774	CTGCCCAACCCAGAGAGAGAGGTTCAGCTGTAAATGTGCCAGGACCAGAGACCGAGAT	833
OY	221	ValGluaIaGlnLeuAraArgLeuGlnGluGluValGlyThrCysLysValCylSleuSpArg	240
Dd	834	GTGAGAGCGCGACTCTCGCGCGCTGCAGAGAGAGAGAGCTGCAGAGTGTGCTTGAACCG	893
OY	241	AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly	260
Dd	894	GCGGTGTCATCGTCTTTGTGCGCGGCGACCTGATCTGTGCTGAAGTAGTCCCCCGGC	953
OY	261	LeuGlnLeuCysProIleCysAraGlaProValAraGserAraGValAraThrPheLeuSer	280
Dd	954	CTGCAGCTGTGCCCATCTGCAGAGACCCCGTCGACCGCGTGCACCTTCTGTCC	1013
RESULT 6			
AFJ11388			
LOCUS	AFJ11388	1260 bp mRNA linear PRI 29-JAN-2001	
DEFINITION	Homo sapiens livin inhibitor-of-apoptosis (LIVIN) mRNA, complete cds.		
ACCESSION	AFJ11388		
VERSION	AFJ11388.1 GI:11245452		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1260) Kasof,G.M. and Gomes,B.C. Livin, a novel inhibitor of apoptosis protein family member J. Biol. Chem. 276 (5), 3238-3246 (2001) 11024045 2 (bases 1 to 1260) Kasof,G.M. and Gomes,B.C. Direct Submission Submitted (05-Oct-2000) Enabling Science and Technology, AstraZeneca Pharmaceuticals, 1800 Concord Pike, Wilmington, DE 19803, USA		
FEATURES			
source	Location/Qualifiers 1..1260 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" 1..1260 /gene="LIVIN" 174..1016 /gene="LIVIN" /note="inhibitor-of-apoptosis family member; contains BIR and COOH-terminal RING finger domains" /codon_start=1 /product="livin inhibitor-of-apoptosis" /protein_id="AAG31622.1" /db_xref="GI:11245453" /translation="MGPKDSAKCLHRGPQSPMAADGPTQERCGPSRLSGVPLDLDTCRAMDHVGQILGLRPLTEEESEAGATLSRPAFGMSSELRLASFYDMDLTLAEVPPELLAAGFPFHGHODXKRCFCYGSLGSKRGDDPWTHAKWPCOFILASKRGRDNFVSVDETHSQLGSNDPMWEPEEDAPAVASVASGYPELPTRREVOSSADEPGADRVAQLRRLOERTCKVCLDRRAVSIVFPCGHLVCABCAPGLDLCPCRAPVRSVRFTFLS"		
gene			
CDS			
ORIGIN			
Alignment Scores:			
Pred. No.:	4.88e-272	Length:	1260
Score:	280.00	Matches:	280
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Gap Match:	90.6%	Indels:	0
DB:	8	Gaps:	0

[illegible]

Dowd, P., Batton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E., Heidens, S., Huang, A., Kim, H.S., Klimoweki, U., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robble, E., Sanchez, C., Scheinfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Steinson, J., Vagstad, A., Vandlen, R., Matanabe, C., Weand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source
1. .1301
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA142232"
1. .1301
/locus_tag="UNQ5800"
215. .1057
/locus_tag="UNQ5800"
/note="PRO19607"
/codon_start=1
/product="LIVIN"
/protein_id="AA089194.1"
/db_xref="GI:37182788"
/translation="MGPKDSAKLHRGPQSHWAGDGPRTORCCGRSLGSPVLLDT
/translating="MGPKDSAKLHRGPQSHWAGDGPRTORCCGRSLGSPVLLDT
VRPELLAAAGFTHTGQDQVPCFPCGCGOSWGRGDDPMTBAKPPSCQFTLRKGR
DFVSHVETHSOLIGSDMPEREDPAAPAPSPVSPGPELTPPREVSESAQEPGA
RDVEAQLRRQRQERTCKVCLDRAVSTVFVPCGLVCAECAPGLDLCPCRAVRSRVR
TFLS"

gene
CDS

Alignment Scores:
Pred. No.: 5,01e-272 Length: 1301
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 8 Gaps: 0

US-09-762-577B-12 (1-309) x AY358835 (1-1301)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
DB 215 ATGGAGACCTTAAGACAGTCCCAAGTCCCGACCGTGGACCAACGAGCCAGCACTGGGCA 274
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 275 GCGGTGATGTCCTCCACGACGAGCGCTGTGACCCCGCTCTCTGGGAGCGCTGTCTTA 334
QY 41 GlyLeuAspThrCysArgAlaTyrPheHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 335 GGCCTGGACACTGACAGACCTGAGACCACTGGAGTGGGAGAGTCTGGCCCACTGGGG 394
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 395 CCCCTGACAG 454
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
DB 455 TTCCCCGCGATGGCTCTGAGGAGTTGGCTCTGGCTCTCTTAATGACTGGCCGCTACT 514
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisTyrGlyYhiGlnAsp 120
DB 515 GCTGAGTGCACCCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574

QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPheArgGlyAspAspPro 140
DB 575 AAGGTAGAGTGTCTTCTGCTATGGGGGCGCTGCAGACCTGGAAGCGCGGAGACGACCCC 634
QY 141 TPTHTGlnHisAlaLeuTyrPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
DB 635 TCGACGAGACATGCCAATGTGTTCCCGACGTGTAGTTCTCTCCGTCCGATCAAAAGAGA 694
QY 161 AppPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrPheProTyr 180
DB 695 GACTTGTTCACAGTGTCCAG 754
QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 755 GAAGAACCAGGAAGACGAGCCCTGTGGCCCTCCCTCCCTGCTGCTGCTGCTGCTGCTG 814
QY 201 LeuProThrProArgTargGluValGlnSerGlnSerAlaGlnGluProGluValArgAsp 220
DB 815 CTGCCACACCCAG 874
QY 221 ValGluAlaGlnLeuArgArgGlyLeuGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGln 240
DB 875 GTGAGGCGGAGCTGCGCGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 934
QY 241 AlaValSerIleValPheValProCysGlyHisIleuValCysAlaGluCysAlaProGly 260
DB 935 GCGGTGTCCATCGCTTGTGTGCGGTGGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 994
QY 261 LeuGlnLeuGlyProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 995 CTGACGCTGTGCCCCATCTGACAGAGCCCGCTGCAGAGCGCGCTGCAGACCTTCTGTCC 1054

RESULT 8
AX067715
LOCUS
DEFINITION
VERSION
ACCESSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
Gomes, B.C., Kasof, G.M. and Prosser, J.C.
Livin; inhibitor-of-apoptosis protein-3 (iap-3)
Patent: WO 0077201-A 1 21-DEC-2000;
Astrazeneca AB (SE)
FEATURES
source
1. .1376
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 5,24e-272 Length: 1376
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) x AX067715 (1-1376)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
DB 211 ATGGAGACCTTAAGACAGTCCCAAGTCCCGACCGTGGACCAACGAGCCAGCACTGGGCA 270
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40

[illegible][illegible]

LOCUS BD185364 672 bp DNA linear PAT 17-JUN-2003
DEFINITION Survivin-like polypeptide and its DNA.
ACCESSION BD185364
VERSION BD185364.1 GI:31877564
KEYWORDS JP 2002355062-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 672)
AUTHORS Tanaka,H. and Kaleda,I.
TITLE Survivin-like polypeptide and its DNA
JOURNAL Patent: JP 2002355062-A 4 10-DEC-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 2002355062-A/4
PD 10-DEC-2002
PF 16-OCT-2001 JP 2001318533
PI HIROSHI TANAKA,ISAO KAIEDA
PC C12N15/09,A61K31/7088,A61K38/55,A61K39/395,A61K48/PC 00,A61P35/00,
A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19,PC C12N1/21,
C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,PC G01N33/53,
G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64 CC Survivin-like polypeptide and its DNA
FH Key location/Qualifiers
FT source 1..672
location/Qualifiers
source 1..672
/organism='Homo sapiens (human)'.
/mol_type='genomic DNA'
/db_xref='taxon:9606'
ORIGIN
Alignment Scores:
Pred. No.: 9.65e-210 Length: 672
Score: 218.00 Matches: 218
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.6% Indels: 0
Gaps: 0
US-09-762-577B-12 (1-309) x BD185364 (1-672)
QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGGGCCCTAAAGACAGTGCCTGACCGTGGACCAAGCCGACGACCCACCTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCGGCGATGATGCCACGACGAGAGCGCTGTGGACCCCGCTCTCTGGGACCCCTTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 121 GGCCTGGACACCTGGACGACCTGGACCACTGGATGGGCAATCGGCGCACGCTGGG 180
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 181 CCCCTGACAG 240
QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyraSPTrpProLeuThr 100
DB 241 TTCCTCCGCGATGCGCTCTGAGAGATTGCTGTGGCTCTCTTAAGTGGCCGCTGACT 300
QY 101 AlaGluValProProGlnLeuLeuAlaIleAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTGAGGTGCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360
QY 121 LysValaArgCysPhePheCysTyrlGlyLeuGlnSerTrpLysArgGlyAspAspPro 140

DB 361 AAGTGAGGTGTTCTTCTGCTATGGGGCCCTGGACGACTGAAAGCGGGGAGACCC 420
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 421 TGGACGGAGCATGCCAAGTGGTTCCCGACGCTGTGCTGTGCTGTGCTGTGCTGTGCT 480
QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 481 GACTTGTCCACAGTGTCCAGAGAGACTCACCACGCTGTGGGCTCTYGGAGCCGTTGG 540
QY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyraSPProGlu 200
DB 541 GAAGAAGCCGAAAG 600
QY 201 LeuProThrProArgArgGlnGlnGlnSerGlnSerAlaGlnGlnGlnGlnGlnGln 218
DB 601 CTGCCACACCCAGAGAGAGAGTCCAGTGAAGTCCCGACGAGCCAGGTGCA 654
RESULT 11
BD167851 723 bp DNA linear PAT 17-JAN-2003
LOCUS BD167851
DEFINITION Survivin-like polypeptide and its DNA.
ACCESSION BD167851
VERSION BD167851.1 GI:27873663
KEYWORDS WO 0233071-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 723)
AUTHORS Tanaka,H. and Kaleda,I.
TITLE Survivin-like polypeptide and its DNA
JOURNAL Patent: WO 0233071-A 3 25-APR-2002;
TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TANAKA,ISAO KAIEDA
COMMENT OS Homo sapiens (human)
PN WO 0233071-A/3
PD 25-APR-2002
PF 16-OCT-2001 WO 2001P009071
PR 17-OCT-2000 JP 00P 316721,20-DEC-2000 JP 00P 386809 PI HIROSHI TANAKA,ISAO KAIEDA
PC C12N15/09,C12N15/12,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/10',C12P21/02,C07K16/18,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,PC A61K31/71,
A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00 CC Survivin-like polypeptide and its DNA
FH Key location/Qualifiers
FT source 1..723
location/Qualifiers
source 1..723
/organism='Homo sapiens (human)'.
/mol_type='genomic DNA'
/db_xref='taxon:9606'
ORIGIN
Alignment Scores:
Pred. No.: 1.02e-209 Length: 723
Score: 218.00 Matches: 218
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.6% Indels: 0
Gaps: 0
US-09-762-577B-12 (1-309) x BD167851 (1-723)
QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGGGCCCTAAAGACAGTGCCTGACCGTGGACCAAGCCGACGACCCACCTGGGCA 60

Oy	21	AlaGlyAspGlyProThrGlnGlnIuArgCysGlyProAsrSerLeuGlySerProValIleu	40
Db	61	GCCGGTATTGCTCCACCGCAGAGGGCTGTGAAACCCGCTCTCTGGGACGCCCTGTCTTA	120
Oy	41	GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg	60
Db	121	GGCTCGGACACCTGCAGAGCTCGGAGCCACGTGGATGGGCAATCCTGGGCCAGCTGGCG	180
Oy	61	ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	80
Db	181	CCCCTGACAG	240
Oy	81	PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr	100
Db	241	TTCCCCGGCATTGGGCTGTGAGGAGTTGGGTCTGGCTCTCTTATATGATCGGCCGCTGACT	300
Oy	101	AlaGlnValProProGlnIuLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp	120
Db	301	GCTGAGGGCCACCCGAGGTGCTGGCTGCTGGCGGCTTCTTCACACAGGCCATCAGAGAC	360
Oy	121	LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysAspGlyLysAspPro	140
Db	361	AAAGTGAGGTGCTTTCTTCTGCTATATGGGGCTTCGACAGCTTGAGAGCGCGGGACGACCCC	420
Oy	141	TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg	160
Db	421	TGGACGGAGCATGCCAAGGTGTTCCCCAGCTTCAGTTCCTCTCCGCTCAAAAGAGAGA	480
Oy	161	AspPheValHisSerValGlnGlnIuThrHisSerGlnLeuLeuGlySerTrpAspProTrp	180
Db	481	GACTTTGTCCACAGTGTGAGAGACTCATCTCCAGCTGTGTGGCTCTYGGGACCCGTGG	540
Oy	181	GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu	200
Db	541	GAGAGACCGGAGAGCGACGCCCTGTGGGCCCTCCGTCCGTGCTTGGTGAACCTTAG	600
Oy	201	LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGluProGlyAla	218
Db	601	CTGCCCAACCCAGAGAGAGAGGTCCAGTCTGAAAGTCCGACAGAGACCGAGTCCA	654
RESULT 12			
BD185363			
LOCUS	BD185363	723 bp	DNA
DEFINITION	Survivin-like polypeptide and its DNA.		linear
ACCESSION	BD185363		
VERSION	BD185363.1		
KEYWORDS	JP 2002355062-A/3.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1 (bases 1 to 723)		
AUTHORS	Tanaka,H. and Kateda,I.		
TITLE	Survivin-like polypeptide and its DNA		
JOURNAL	Patent: JP 2002355062-A 3 10-DEC-2002;		
	TAKEDA CHEMICAL INDUSTRIES LTD		
COMMENT	OS Homo sapiens (human)		
	^ PN JP 2002355062-A/3		
	^ PD 10-DEC-2002		
	PF 16-OCT-2001 JP 2001318533		
	PI HIROSHI TANAKA, ISAO KAIEDA		
	PC C12N15/09,A61K31/7088,A61K38/55,A61K39/395,A61K39/395,A61K48/		
	PC 00,A61P35/00,		
	PC A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19, PC		
	C12N1/21,		
	PC C12N6/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50, PC		
	G01N33/53,		
	PC G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64		
	CC Survivin-like polypeptide and its DNA		
	FH key		
	Location/Qualifiers		
	FT source		
	1..723		
	/organism='Homo sapiens (human)'		

FEATURES		Location/Qualifiers
source		1..723
ORIGIN		/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
Alignment Scores:		
Pred. NO.:	1.02e-209	length: 723
Score:	218.00	Matches: 218
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	70.6%	Indels: 0
DB:	6	Gaps: 0
US-09-762-577B-12 (1-309) x BD185363 (1-723)		
QY	1 MetG1yProLysrPsrSerAlaLysCyLeuNiSaArgG1yProGlnProSerNiStrPaLa	20
Db	1 ATGGGGCTTAAGACAGTCCCAAGTGGCTGACACGTGGACACACAGCCGACCTGGGCA	60
QY	21 A1AG1yAsrG1yProThrGlnGlnLysGyG1yProArgSerLeuG1ySerProValLeu	40
Db	61 GCCGGATGATGCTCCACGACGAGCGCTGTGACCCCGCTCTGGGACCCCTGTCTTA	120
QY	41 G1yLeuAsrThrCysAsrG1aLarPsrNiSaValAspG1yGln1LeuG1yGlnLeuArg	60
Db	121 GGCTTGACACCTGGACAGCTGGACACCTGGATGGGACATCTGGGCGACCTGGG	180
QY	61 ProLeuThrG1uGlnG1uGlnG1uGlnG1yAlaG1yAlaThrLeuSerArG1yProAla	80
Db	181 CCCCTGCAGAGGAGGAAAGGAGGAGGAGGCGCGGCGCCACTTGTCCAGGGGCGCTGC	240
QY	81 PheProG1yMetG1ySerG1uGlnLysArgLeuAlaSerPheTyraSPTrpProLeuThr	100
Db	241 TTCCCGGCAATGGGCTGTGAGAGTGGCGTGTGACCTCTTATGACTGGCGCTGACT	300
QY	101 A1AG1yValProProG1uLeuLeuAlaAlaG1yPhePheNiStrG1yNiGlnAsp	120
Db	301 GCTGAGGTGCACCCGACGCTGTGGCTGTGGCGCTTCTTCCACAGGCGCATCAGAC	360
QY	121 LysValArgCysPhePheCysTyTG1yG1yLeuGlnSerTrpLysArgG1yAspAspPro	140
Db	361 AAGGTGAGGCTTCTTCTTCTTATGGGGGCTGCAGAGCTGAAAGCGGGGAGACCC	420
QY	141 TrpThrG1uNiSaLysTrpPheProSerCysG1yPheLeuLeuArgSerLysG1yArg	160
Db	421 TGGACGAGAGATGCCAAGTGTCTCCCAAGCTGCAGTCTCTCGGTCAAAAGAGA	480
QY	161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuG1ySerTrpAspProTrp	180
Db	481 GACTTGTCCACAGTGTGCAGAGAGACTCTCCACACTGTGTGGGCTCTGGAGACCGGTG	540
QY	181 GlnGlnProG1uAspAlaAlaProValAlaProSerValProAlaSerG1yTyProGln	200
Db	541 GAAGAAACCGAAGACGACGCCCTGTGGCCCCCTTCGCTCTCTGGGTACCTTGAG	600
QY	201 LeuProThrProArgTrgG1uValGlnSerG1uSerAlaGlnGlnProG1yAla	218
Db	601 CTGCCCCACACCGAGAGAGAGTCCAGTGTGAAGAGGCCAGAGACGAGGTGCA	654
RESULT 13		
LOCUS	AF301009	
DEFINITION	AF301009 Homo sapiens inhibitor of apoptosis protein KIAA complete cds.	
ACCESSION	AF301009	
VERSION	AF301009.1	
KEYWORDS	GI:11545502	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	

REFERENCE
1 (bases 1 to 1168)
Hominidae; Homo.
AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 1168)
AUTHORS
TITLE
JOURNAL
Submitted (29-AUG-2000) Cardiovascular Research, Berlex Biosciences Inc., 15049 San Pablo Ave., Richmond, CA 94804, USA

FEATURES
Source
1. .1168
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="20"
/map="20q13.3"
/tissue_type="kidney"
/dev_stage="fetus"
1. .897
/codon_start=1
/product="inhibitor of apoptosis protein KIAP"
/protein_id="A037878.1"
/db_xref="GI:11545503"
/translation="MGPKDSAKCLHRGPQSHMAAGDPTORCGPRISGEPVLGIQDT
CRAMHDVQQLIGQLPLTEEBEGAGTSLRGPAPGMSSEELRLASFYMPILTA
VPELLAAGFFHTGHODVRCPCFGYGLQSMKRDPPWTHAKKPFSCQFLRSKGR
DFVHSYQETHTSGLGSDMPMBEEDAPVAPSPVAPSGFELTTPREVQSSADSPGG
VSPAEQKRAWMVLEPPGARDVEMQRLRLOERTCKVCLDRAVSIVFVPGHLYCAEA
PGIQLQICRAIPRSRVRTFLS"
259. .462
/note="Region: BIR domain"
721. .867
/note="Region: RING domain"

ORIGIN
Alignment Scores:
Pred. No.: 1.55e-208 Length: 1168
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x AF301009 (1-1168)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGGACCTAAAGACAGTGCCTCAAGTGCCTGCACCGTGCACACAGCCGACCTGGGCA 60

QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCGGATGATGTCCTCCACGACGAGGAGGCTGTGACCCCGCTCTCTGGGACCCCTTCTTA 120

QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 121 GGCCTGGACACTGCAGACCTGCAGACCACTGCAGTGGGACAGATCTGGGACAGTGGCG 180

QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 181 CCCCTGACAG 240

QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 241 TTCCCCGGGATGGCTGTGAGGAGTTGGCTGGCTCTCTTAAGACTGGGCGCTGACT 300

QY 101 AlaGluValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTTGGAGGACACCCGAGCTGCTGCTGCTGCTGCTGCTTCTTCCACACAGGCCATCAGGAC 360

QY 121 LysValAlaGlyCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 361 AAGGAGAGTGTCTTTCTGCTATGGGGGCTTGCAGAGCTGMAAGCGGGAGAGAGACCCC 420

QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
DB 421 TGGAGGAGCATGCCAATGGTTCCTCCAGCTGTCACTTCTGCTCCGGTCAAAAAGAGA 480

QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 481 GACTTTGTCCACAGTGTGCAGAGAGACTCATCCACAGCTGTGGGCTCTTGGGACCCGTGG 540

QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 541 GAAGAACCGGAAGACGAGCCCTGTGGCCCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlnProGly 217
DB 601 CTGCCACACCCACAGAGAGAGAGTCCAGTCTGAAGTGTCCAGGCCAGGACGAGGA 651

RESULT 14
LOCUS CQ896990 1312 bp DNA linear PAT 08-NOV-2004
DEFINITION Sequence 10 from Patent WO2004091388.
ACCESSION CQ896990
VERSION CQ896990.1 GI:55581832
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Butz, K., Crnkovic-Wertens, I. and Hoppe-Seyler, F.
TITLE LVIIN-SPECIFIC siRNAs FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS
JOURNAL Patent: WO 2004091388-A 10 28-Oct-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)

FEATURES
Location/Qualifiers
1. .1312
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.7e-208 Length: 1312
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x CQ896990 (1-1312)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 149 ATGGGACCTAAAGACAGTGCCTCAAGTGCCTGCACCGTGCACACAGCCGACCTGGGCA 208

QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 209 GCGGATGATGTCCTCCACGACGAGGAGGCTGTGACCCCGCTCTTGGGACAGCCCTTCTTA 268

QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 269 GGCCTGACACCTGCAGAGAGCTGGACACAGTGGATGGCAATCTTGGGCGAGCTGGCG 328

QY 61 ProLeuThrGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 329 CCCCTGACAG 388

QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 389 TTCCCCGGGATGGCTGTGAGGAGTTGGCTGGCTCTCTTAAGACTGGGCGCTGACT 448

QY 101 AlaGluValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120

Db 449 GCTGAGTCCACCCGAGCTGTGCTCTGCTGCGCTCTTCCACACGCGCATAGGAC 508
Qy 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPlyArgGlyAspAspPro 140
Db 509 AAGGTGAGGTGCTCTTCTTGTGCTATGGGGCTCGACAGCTGGAAGCGGGGACGACCC 568
Qy 141 TTPThrGluHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerTyrGlyArg 160
Db 569 TGGACGGGAGCATGCCAAGTGTGCTCCCGCTGCTGCTGCTCCGCTCAAAAGGA 628
Qy 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuGlnSerTyrAspProThr 180
Db 629 GACTTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGTGGGTCTCTGGACCCGG 688
Qy 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 689 GAAGAACCGGAAGACGACGCCCTGTGGCCCTCCCTGCTGCTGCTGCTGCTGCTGAG 748
Qy 201 LeuProThrProAlaArgGlyValGlnSerGlnSerAlaGlnGluProGly 217
Db 749 CTGCCACACACCGAGAGAGAGAGTCCAGTCTGAAGTGCACGAGCAGCA 799
RESULT 15
LOCUS BC014475 1312 bp mRNA linear PRI 30-JUN-2004
DEFINITION Homo sapiens baculoviral IAP repeat-containing 7 (Iivin),
transcript variant 1, mRNA (cDNA clone MGC:23131 IMAGE:4859588),
complete cds.
ACCESSION BC014475
VERSION BC014475.1 GI:15680240
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1312)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heist,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheez,T.E., Brownstein,M.J., Ubedin,T.B., Toshlyuk,I.S.,
Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Vitalion,D.K., Wuzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bonfield,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,J.S., Krzywinski,M.I., Skalska,U., Smalins,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
TITLE
JOURNAL PUBMED 12477932
REFERENCE
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/CDTD/DTF
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherston, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Liao,
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabh,
Parvaneh Saeedi, JR Santos, Angeliq Schnerch, Ursula Skalska,
Duane Smalins, Jeff Scott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 34 Row: 6 Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21536419.
FEATURES
Source
1..1312
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:23131 IMAGE:4859588"
/tissue_type="Skin, melanotic melanoma, high MDR."
/clone_id="NIH_MGC_49"
/lab_host="DH10B-R"
/note="Vector: POTB7"
1..1312
/gene="BIRC7"
/note="Synonyms: ML-IAP, KIAP, LIVIN, RNF50, MLIAF"
/db_xref="GeneID:79444"
/db_xref="MIM:605737"
149..1045
/gene="BIRC7"
/codon_start=1
/product="Iivin inhibitor of apoptosis, isoform alpha"
/protein_id="AAH14475.1"
/db_xref="GI:15680241"
/db_xref="MIM:605737"
/translation="MGPKDSAKCLHGRPOSHWAAGDPGROEGRPSLSPVGLDT
CRMADVDQIIQLRLPLTEEEEGAGPLTSGAPPGMGSEELRLASPYDPLTAE
VPPELLAAAFPHTHGDKRCFCFCGLOSFKRGDDPTWTEHAKWFPSCPLBSKR
DPAHVSDETHSGLSDPWEPEEDAPVAPSPASGPELPPTPREVQSESAQPCG
VSPAQAGRAMVWLEPPGARDVEALRLDERTCKVCLDRAVSVIFVPCGHLVCAECA
PGLQICPICAPRPSRRTPLS"
ORIGIN
Alignment Scores:
Pred. No.: 1,7e-208 Length: 1312
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
DB: 8 Gaps: 0
US-09-762-577b-12 (1-309) x BC014475 (1-1312)
Qy 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db 149 ATGGGACCTTAAGACATGCGCAAGTGCCTCACCAGTGAGCACACGCGAGCCTGGGCA 208
Qy 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlnSerProValLeu 40
Db 209 GCCGTATGTCCTCCACGACGAGCGGTGTGAGACCCCGCTCTCTGGGACGCTGTCTTA 268
Qy 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlnIleuArg 60
Db 269 GGCTTGACACCTTGCAAGCCTGGGACCACTGATGGAGAGTCTTGCGGCGAGCTTCGG 328
Qy 61 ProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db 329 CCCTGACAG 388

```
QY      81 PheProGlyMetGlySerGluGluLeuAlaSerPheTyrAspTyrProLeuThr 100
Db      389 TTCCCGGCGATGGGCTCTGAGAGAGTTGGCTGGCCCTCTTATGACTGGCCGCTGACT 448
QY      101 AlagluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      449 GCTGAGGTGGCCACCCGAGCTGTGGCTGTGCCGCTTCTCCACACAGGCCATCAGAGAC 508
QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      509 AAGGTGAGGTGCTTCTTCTGCTATGGGGGCTGCAGAGCTGGAAGCGCGGAGCAGACCCC 568
QY      141 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      569 TGGACGAGAGCATGGCCAAAGTGATGCCAGCTGTCAAGTCTCTCGCTCCGATCAAAAGGAGA 628
QY      161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTyr 180
Db      629 GACTTGTCTCCACAGTGTGCAGAGACTCACTCCACAGCTGTGGGCTCTGGAGACCGTGG 688
QY      181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db      689 GAAGAACCGGAAAGACGAGCCCTGTGGCCCTCCGCTCTGCTGTGGTACCTCTGAG 748
QY      201 LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGly 217
Db      749 CTGCCCAACCCAGAGAGAGGTCCAGTCTGAAGAGTCCCAAGAGCCAGGA 799
```

Search completed: April 24, 2006, 11:57:50
Job time : 4452 secs

GenCore version 5.1.7
(c) 1993 - 2006 Biocore

ic search, using frame_plus_p2n model

April 24, 2006, 09:59:41 ; Search time 733 Seconds

2809.536 Million cell updates/sec

SS-09-762-577B-12

MGPKDSAKCLHRGPQPSHWA.....GLQGLPAPLCLFWTVFWAC 309

gagap	60.0	Xgapext	60.0
gagap	60.0	Ygapext	60.0
gagap	60.0	Fgapext	7.0
elap	60.0	Delext	60.0

996997 seqs, 3332346308 residues

its satisfying chosen parameters: 9989204

```
length: 0
length: 20000000000
```

Listing first 45 summaries

meters:

```

T=fastab -SUFFIX=2pmol1.rmg -MINMATCH=0.1 -LOOPC=0
-bits -START=1 -END=1 -MATRIX=1 -TRANS=mode40.cdi
-THR SCORE=quality -THR MIN=1 -ALIGN=15 -MOD=LOCAL
next -HAP35=5500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abseq03h3
CCN 1 1 727 @unac 24042006 105917 662 NCRU=6 -ICP=0.3
WAIT -DSBBLCK=100 -JONGIG -DEV TIMEOUT=120
THRAD=1 -XGAP=60 -XCAPTEXT=60 -FGAP=60 -FCAPTEXT=7
=60 -DELXT=60

```

GeneSeq_21: *

```

1:  geneseqn1980s: *
2:  geneseqn1990s: *
3:  geneseqn2000s: *
4:  geneseqn2001as: *
5:  geneseqn2001bs: *
6:  geneseqn2001as: *
7:  geneseqn2002as: *
8:  geneseqn2002bs: *
9:  geneseqn2003as: *
10: geneseqn2003bs: *
11: geneseqn2003cs: *
12: geneseqn2003ds: *
13: geneseqn2004as: *
14: geneseqn2004bs: *
15: geneseqn2004bs: *
16: geneseqn2005a: *

```

is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, divided by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
100.6	840	6	AA143858	AA143858	Survivin
100.6	843	4	AA124857	AA124857	Nucleotid
100.6	1260	12	ADH89535	ADH89535	Human Liv
100.6	1260	14	AEA36171	AEa36171	Human nuc

5	280	90.6	1268	10	ACC72844	Human	can
6	280	90.6	1268	13	AD571346	Human	liv
7	280	90.6	1376	4	AAFP24856	Nucleotid	
8	218	70.6	672	6	AA142857	Survivin-	
9	218	70.6	733	6	AA142856	Survivin-	
10	217	70.2	1168	12	ADH89543	Human	liv
11	217	70.2	1332	10	ACC72843	Human	liv
12	217	70.2	1332	13	AD571344	Human	can
13	217	70.2	1337	3	AAZ61210	Human	liv
14	217	70.2	1353	3	AAAI5007	DNA	encod
15	217	70.2	1353	13	ADT86075	DNA	enco
16	177	57.3	1068	4	AAAD16344	Human	pro
17	149	48.2	449	12	ADQ21877	Human	SBH
18	149	48.2	769	4	AAAD16365	Human	sof
19	131	42.4	858	12	AAAD25445	Human	SBH
20	120	38.8	614	5	AAAS1550	Human	sof
21	120	38.8	615	4	AAAH92228	DNA	encod
22	117	37.9	4780	12	ADH89542	Human	pro
23	116	37.5	3782	5	AAAS1553	Human	liv
24	87	28.2	339	14	AAEA39481	DNA	encod
25	68	22.0	204	6	AAAL42854	Human	ML-
26	65	21.0	676	12	ADQ21628	Survivin-	
27	54	17.5	404	5	AAFE66650	Human	sof
28	47	15.2	141	6	AAAL42855	Novel	hum
29	44	14.2	226	11	AD131008	Survivin-	
30	44	14.2	226	13	AD5830375	Human	CDN
31	30	9.7	200	10	ACAS55618	Human	lym
32	30	9.7	200	11	AD131061	Mouse	sig
33	30	9.7	200	12	AD155414	Human	CDN
34	30	9.7	200	13	AD583128	Human	pol
35	28	9.1	444	5	AAAS1551	Human	lym
36	21	6.8	121	10	ADH93056	DNA	encod
37	18	5.8	1531	10	ADP17464	Human	gen
38	15	4.9	539	13	ADOS15193	Mouse	IL-
39	14	4.5	363	10	AD032333	Novel	can
40	14	4.5	460	8	ABX42864	Human	mit
41	14	4.5	1435	2	AAAT3709	Bovine	ES
42	14	4.5	1601	11	AD131171	Human	inh
43	14	4.5	1601	13	AD583238	Human	CDN
44	14	4.5	1657	14	AAE17853	Human	lym
45	14	4.5	2416	2	AAAT70841	Mouse	inh
						apo	

ALIGNMENTS

LT 1
2858
AAL42858 standard; DNA; 840 BP.

AA142858;

05-AUG-2002 (first entry)

Survivin-like protein coding sequence 5.

Survivin-like protein; diagnosis; screening; cancer; gene; ds;

1. *Chlorophyll a* (Chl a) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl a is essential for the light-dependent reactions of photosynthesis, where it converts light energy into chemical energy in the form of ATP and NADPH. The structure of Chl a consists of a central magnesium atom coordinated by four nitrogen atoms in a porphyrin-like ring, with a long phytol side chain attached to one of the ring carbons.

CDS	1. .840
-----	---------

/partial

```
/note= "No stop codon is given"
```

WO200233071-A1.

25-APR-2002.

16-OCT-2001; 2001WO-JP009071.

```

PR 17-OCT-2000; 2000JP-00316721.
PR 20-DEC-2000; 2000JP-00368809.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Tanaka H, Kaieda I;
XX
XX WPI; 2002-435536/46.
XX P-PSDB; AAO14947.
XX
XX Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
XX like polypeptides and encoded DNAs, applicable in diagnosis and screening
XX compounds for treating various cancers and apoptosis abnormality.
XX
XX PS Disclosure; Page 122; 136pp; Japanese.
XX
XX CC The invention comprises the amino acid and coding sequences of survivin-
XX like proteins. The survivin-like DNA and protein sequences are useful in
XX diagnostics and screening compounds for treating various cancers and
XX apoptosis abnormality, including gene therapy. The present DNA sequence
XX encodes a survivin-like protein of the invention
XX
SQ Sequence 840 BP; 136 A; 272 C; 287 G; 144 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.5e-257 Length: 840
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: Gaps: 0

US-09-762-577B-12 (1-309) x AAL42858 (1-840)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 1 ATGGGGCTTAAGACAGTGCCTGACCGTGGACACAGCCGACCTGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 61 GCCGGTGAATGTCCTCCAGCAGAGAGCGCTGTGGACCCCGCTCTCTGGGACCCCTTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 121 GGCCTGGAACCTGCGAGACCTGGGACACGATGGATGGGCAATCCTGGCCAGCTGGCG 180
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 181 CCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 241 TTCCCGCGGATGGGCTCTGAGAGATGGCTGTGGCTCTCTCTATGATCTGGCCCGCTGACT 300
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlnPhePheHisThrGlnHisGlnAsp 120
Db 301 GCTGAGGTCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 121 LysValAlaGlyCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db 361 AAGGTAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 141 TrpTrpGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
Db 421 TGGAGCGGATGCCAAGTGTTCCTCCAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 161 AspPheValHisSerValGlnGlnHisSerGlnLeuLeuGlnGlnGlnGlnGlnGlnGln 180
Db 481 GACTTTGTCCACAGTGTCCAGAGACTCACTCCAGCTGCTGGGCTCTTGGGACCCGTTGG 540
QY 181 GlnGluProGlnLysAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
Db 541 GAAGAACCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

```

```

QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlnProGlnValAlaArgAsp 220
Db 601 CTGCCCAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 661 GTGAGGCGCAGCTGCGCGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
Db 721 GCGGTTCATCGTCTTTGTGCTGTGGCCACCTGTCTGTGTGAGTGTGCCCCCGCGC 780
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 781 CTGCAGCTGTCCCACTGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

RESULT 2
AAF24857
ID AAF24857 standard; cDNA; 843 BP.
XX
XX AAF24857;
XX
XX 20-APR-2001 (first entry)
XX
XX DE Nucleotide sequence of an apoptosis inhibitor designated livin.
XX
XX XX Livin; apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;
XX
XX XX melanoma; Alzheimer's disease; Parkinson's disease; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 1..843
XX FT /*tag= a
XX FT /product= "livin"
XX
XX PN MO200077201-A1.
XX
XX PD 21-DEC-2000.
XX
XX PF 09-JUN-2000; 2000MO-GB002272.
XX
XX PR 15-JUN-1999; 99US-0139291P.
XX
XX PA (ASTR ) ASTRAZENECA AB.
XX PA (ASTR ) ASTRAZENECA UK LTD.
XX
XX PI Gomes BC, Kasof GW, Prosser JC;
XX
XX DR WPI; 2001-122843/13.
XX DR P-PSDB; AAB31478.
XX
XX PT Novel livin polypeptides and polynucleotides useful for treating
XX PT pathophysiological disorders related to apoptosis, cancers, particularly
XX PT melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene
XX PT therapy.
XX
XX PS Claim 8; Page 54; 62pp; English.
XX
XX XX The present sequence encodes a human polypeptide, designated livin. Livin
XX CC is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in
XX CC certain cancer cell lines and prevents apoptosis. The livin polypeptide
XX CC is useful for identifying compounds that inhibit and modulate livin
XX CC function and activity. Such compounds are useful in the treatment of a
XX CC dysfunctional apoptosis condition. Livin polypeptides are useful as a
XX CC source of probes and primers, and in gene therapy. Livin polypeptides and
XX CC polynucleotides, their inhibitors and modulators are useful for treating
XX CC pathophysiological disorders related to apoptosis, cancers, particularly
XX CC melanoma cancer, Alzheimer's disease and Parkinson's disease
XX
XX SQ Sequence 843 BP; 138 A; 273 C; 287 G; 145 T; 0 U; 0 Other;

```

Alignment Scores:

Pred. No.: 2.5e-257 Length: 843
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 4 Gaps: 0

US-09-762-577B-12 (1-309) x AAF24857 (1-843)

OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGGACCTTAAGACAGTGCCTGAGGAGTGCCTGACCTGTGACCAACAGCCAGCCACCTGGCA 60
OY 21 AlaGlyAspGlyProThrGlnGlnIuArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCCGGTGAATGCTCCACAGCAGAGGCGCTGTGAGCCCGCTCTCTGGGAGCCCTGTCTCA 120
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 121 GGCTTGACACCTGACAGAGCTGGGACCACTGATGGGAGATCTGGGACAGCTGGCG 180
OY 61 ProLeuThrGlnGlnGlnIuArgGlnIuArgGlnIuArgAlaThrLeuSerArgGlyProAla 80
DB 181 CCCCTGACAG 240
OY 81 PheProGlyMetGlySerGlnGlnIuArgLeuArgLeuAlaSerPheTyAspTrpProLeuThr 100
DB 241 TTCCCGGCGCATGGGCTGTGAGGAGTGGCTGGCTGGCTCTCTTAAGACTGGCGCGTGA 300
OY 101 AlaGlyValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTGAGGAGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
OY 121 LysValArgCysPhePheCysTyArgGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 361 AAGGTGAGGTGCTTCTTCTGCTATGGGGGCTGCGAGACTGAGAGCCGGGGAGCAACCC 420
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerIleValArg 160
DB 421 TGGACGAGCATGTCAGAGTGGTCCCGCAGCTGTCACTTCTGCTCGGTCAGAAAGAGAGA 480
OY 161 AspPheValHisSerValGlnGlnIuThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 481 GACTTGTCCACAGTGCAGAGAGACTCACTCCAGCTGGGCTGCTGGAGACCCGCTGG 540
OY 181 GlnIuProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyProGln 200
DB 541 GAAGAACCGAAGACGAGCCCTGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 600
OY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnIuProGlyAlaAsp 220
DB 601 CTGCCACACCCAGAGAGAGAGAGTCCAGTCTGAAAGTGCAGAGAGCCAGAGCCAGGAT 660
OY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnIuArgThrCysIleValCysLeuAspArg 240
DB 661 GTGAGGGGCGAGCTGGCGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
OY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
DB 721 GCCGTGTCATCGTCTTGTGCTGCGGCGGCACTGGTCTGTGCTGATGTGCCCCCGGC 780
OY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 781 CTGCGAGCTGTGCCCATCTGCAGAGAGCCCGGCTGCCAGCCGCGTGGCAGCCCTTCTGTC 840

RESULT 3

ADH89535 standard; DNA, 1260 BP.

ADH89535;

22-APR-2004 (first entry)

XX Human Livin DNA.

DE hyperproliferative disorder; aberrant apoptosis; human; ds; Livin; gene.
XX
KW Homo sapiens.
XX
OS US2004005565-A1.
XX
FN 08-JAN-2004.
XX
PD 02-JUL-2002; 2002US-00188646.
XX
PE 02-JUL-2002; 2002US-00188646.
XX
PR 02-JUL-2002; 2002US-00188646.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KM;
XX
XX WPI; 2004-098436/10.
DR P-PSDB; ADH89685.
XX

PT New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
PT
XX

XX Example 13; SEQ ID NO 4; 60pp; English.

XX The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding Livin and that specifically hybridises with the nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The present sequence represents human livin DNA.
XX

SQ Sequence 1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.62e-257 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 12 Gaps: 0

US-09-762-577B-12 (1-309) x ADH89535 (1-1260)

OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 174 ATGGGACCTTAAGACAGTGCCTGAGGAGTGCCTGACCTGTGACCAACAGCCAGCCACCTGGCA 233
OY 21 AlaGlyAspGlyProThrGlnGlnIuArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 234 GCCGGTGAATGCTCCACAGCAGAGGCGCTGTGAGCCCGCTCTCTGGGAGCCCTGTCTCA 293
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 294 GGCTTGACACCTGACAGAGCTGGGACCACTGATGGGAGATCTGGGACAGCTGCGG 353
OY 61 ProLeuThrGlnGlnGlnIuArgGlnIuArgGlnIuArgAlaThrLeuSerArgGlyProAla 80
DB 354 CCCCTGACAG 413
OY 81 PheProGlyMetGlySerGlnGlnIuArgLeuArgLeuAlaSerPheTyAspTrpProLeuThr 100
DB 414 TTCCCGGCGCATGGGCTGTGAGGAGTGGCTGGCTGGCTCTTCTTAAGACTGGCGCGTGA 473
OY 101 AlaGlyValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 474 GCTGAGGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
OY 121 LysValArgCysPhePheCysTyArgGlyLeuGlnSerTrpLysArgGlyAspAspPro 140

Db 534 AAGGTGAGGTGCTTCTTCTGCTATGAGGGGCTGCAGAGCTGGAAGCGGGGAGAGACCC 593
 Qy 141 TTTTThTlNHhAlaIySTrPheProSerCySglnPheLeuLeuArySerLySgIyAry 160
 Db 594 TGGACGGACAGCCAGAGGTGTCCCGAGCTGTGATTCCTGCTCCGTCMAAGAGAGA 653
 Qy 161 AAPPheValHieSerValGlnGlnThrhHsserGlnLeuGlySerTTPAspProTrp 180
 Db 654 GACTTTGTTCACAGTGTGAGAGAGCTCACTCCAGCTGTGGGCTCTGGGAGCCCTGG 713
 Qy 181 GlnGlnProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTTPProGlu 200
 Db 714 GAAGAAGCGGAAGAGAGAGCCCTGTGGCCCTCCCTGCTGCTGAGTACCTCTGAG 773
 Qy 201 LeuProThrProAryAryGlnValGlnSerGlnSerAlaGlnGlnProGluAlaAryAsp 220
 Db 774 CTGCCACACCCAGAGAGAGGTCCAGCTTAAAGTCCACAGAGAGAGAGAGAGAT 833
 Qy 221 ValGlnAlaGlnLeuAryAryLeuGlnGlnThrhCysAlaValCysLeuAryAry 240
 Db 834 GTGAGAGCGAGCTGCGCGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
 Qy 241 AlaValSerIleValPheValProCysGlyHieLeuValCysAlaGlnCysAlaProGly 260
 Db 894 GCGGTGTTCATCGTCTTGTGTCCGTGGGCGCACCTGTGTGTGTGTGTGTGTGTGTGT 953
 Qy 261 LeuGlnLeuCysProIleCysAryAlaProValArySerAryValAryThrPheLeuSer 280
 Db 954 CTGACAGGT 1013

RESULT 4

AE36171
ID AE36171 standard; DNA, 1260 BP.

AC AEA36171;

DT 25-AUG-2005 (first entry)

XX Human nucleic acid sequence #103.

KM Screening; gene expression; colorectal tumor; colitis; Crohn's disease;
 KW Irritable bowel syndrome; gastrointestinal disease; cytostatic;
 KM Gastrointestinal-gen.; antiinflammatory; ds.

OS Homo sapiens.

XX MO2005054507-A2.

XX 16-JUN-2005.

XX 03-DEC-2004; 2004WO-GB005078.

XX 04-DEC-2003; 2003GB-00028048.

XX (UYSH-) UNITV SHEPFIELD.

XX Corfe B, Chirakkal H;

XX WPI; 2005-435407/44.

PT Screening for nucleic acid molecules exhibiting altered expression in
 PT cells grown in the presence of butyrate, and detection of the nucleic
 PT acid molecules or the encoded polypeptides in diagnosing colorectal
 PT cancer.

XX Disclosure; Page 143; 266pp; English.

CC The invention relates to a method of screening for nucleic acid molecules
 CC that show altered expression in a first cell sample comprising comparing
 CC the gene expression profile of the sample with that of a second reference
 CC sample, where the first sample has been grown in the presence of butyrate
 CC or a related carbon source from which butyrate is directly or indirectly
 CC derived, but the reference sample has not. The invention also relates to

CC a method of detecting at least one nucleic acid molecule associated with
 CC the initiation and/or progression of colorectal cancer in an animal,
 CC comprising providing a biological sample comprising at least one cell to
 CC be tested, contacting the sample with a ligand (preferably a hybridizing
 CC nucleic acid molecule) which binds to at least one nucleic acid and
 CC detecting the presence of at least one molecule in the sample, a method
 CC of detecting at least one polypeptide associated with the initiation
 CC and/or progression of colorectal cancer in an animal comprising providing
 CC a biological sample comprising at least one cell to be tested, contacting
 CC the sample with at least one ligand that specifically binds at least one
 CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising
 CC an amino acid sequence which varies by the addition, deletion or
 CC substitution of at least one amino acid residue and detecting the
 CC presence of the polypeptide in the sample, a method of screening for
 CC agents that modulate the activity of at least one polypeptide encoded by
 CC a gene associated with the initiation and/or progression of colorectal
 CC cancer comprising forming a preparation comprising at least one
 CC polypeptide encoded by a nucleic acid or a variant polypeptide comprising
 CC at least one addition, deletion or substitution and at least one agent to
 CC be tested and determining the activity of the agent with respect to
 CC activity of the polypeptide, and an antibody or its effective binding
 CC portion identified by the method, for use as a pharmaceutical. The
 CC methods are useful for screening for nucleic acid molecules that show
 CC altered expression in a cell sample, and for detecting a nucleic acid
 CC and/or polypeptide respectively, that are associated with the initiation
 CC and/or progression of colorectal cancer and are useful for detecting or
 CC monitoring colorectal cancer, especially adenocarcinoma. The methods are
 CC also useful for screening for agents that modulate the activity of at
 CC least one polypeptide encoded by a gene associated with the activity of at
 CC and/or progression of cancer, where agents identified by the method are
 CC useful for treating colorectal cancer. The methods could also be used to
 CC detect or monitor other conditions such as colitis, Crohn's disease or
 CC irritable bowel syndrome, as a screening tool for fiber consumption, as
 CC an assay for colon microflora functionality or for early detection of pre
 CC -cancerous growth. This sequence represents a human nucleic acid
 CC identified by the screening method of the invention.

SO Sequence 1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3, 62e-257 Length: 1260
 Score: 280.00 Matches: 280
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 90.6% Indels: 0
 DB: 14 Gaps: 0

US-09-762-577B-12 (1-309) x AEA36171 (1-1260)

Qy 1 MetGlyProIlyAAspSerAlaIySyluHlsarGlyProGlnProSerHlsTrpAla 20
 Db 174 ATGGAGCTTAAAGACAGAGGCCAAGTGCCTGCACCGTGCACAGAGCCAGCATGGGCA 233
 Qy 21 AlaGlyAspGlyProThrGlnGlnAryGlyProArySerLeuGlySerProValLeu 40
 Db 234 GCCGGTGAATGTCACACCAAGAGAGGCTGTGACCCCGCTCTGGGAGAGCCGTCTTA 293
 Qy 41 GlyLeuAspThrCysAryAlaTrpAspHlsValAspGlyGlnIleLeuGlyGlnLeuAry 60
 Db 294 GGCCTGGACACCTGCAGAGCTGGGACACAGTGAATGGGAGATCTGGGCGAGCTCGG 353
 Qy 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 Db 354 CCCCTGACAG 413
 Qy 81 PheProGlyMetGlySerGlnGlnLeuAryGlnLeuArySerPheTyraPTrpProLeuThr 100
 Db 414 TTCCCGGCGCATGGGCTGTGAGAGTTCGTGCTGCGCTCTTCTATAGCTGGCCGCTGACT 473
 Qy 101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHlsThrGlyHlsGlnAsp 120
 Db 474 GCTAGAGTGCACCCGAGCTGTGGCTGTGGCTTCTTCACACAGGCCATCAGAGAC 593

QY 201 LeuProThrProAlaGArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220
 Db 774 CTGCCACACCCAGAT 833
 QY 221 ValGluAlaGlnLeuArgArgLeuGlnGluGlnArgThrGlyValCysLeuAspArg 240
 Db 834 GTGAGAGGCGCAGCTCGCGCGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
 QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
 Db 894 GCCGTGTCATCGCTCTTGTCCTGCGCGCAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 953
 QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 Db 954 CTGCAGCTGTGCCCACTGCAG 1013

RESULT 6
 AD571346
 ID AD571346 standard; DNA; 1268 BP.
 AC AD571346;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human livin beta splice variant DNA.
 XX
 KW Immune response; cancer-associated Inhibitor of Apoptosis-family protein;
 KM IAP-family protein; cancer; lung cancer; colorectal cancer; melanoma;
 KM human, livin beta; gene; ds; immunostimulant; cytostratic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 174..1016
 FT /tag= a
 FT /product= "Human livin beta splice variant protein"
 XX
 PN US2004192631-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 24-MAR-2004; 2004US-00807897.
 XX
 PR 24-MAR-2003; 2003US-0457009P.
 XX
 PA (XIAN/) XIANG R.
 PA (ZHOU/) ZHOU H.
 PA (REIS/) REISFELD R. A.
 XX
 PI Xiang R, Zhou H, Reisfeld RA;
 XX
 DR MPI; 2004-689881/67.
 DR F-PSDB; AD571347.
 DR REFSEQ; NM_022161.
 XX
 PT New DNA vaccine comprising a cancer-associated Inhibitor of Apoptosis-
 PT family protein immunoreactive gene product, useful for eliciting an immune
 PT response against cancer.
 XX
 PS Claim 26; SEQ ID NO 28; 84bp; English.
 XX
 CC The present invention relates to a DNA vaccine effective for eliciting an
 CC immune response against cancer cells which comprises a DNA construct
 CC operably encoding at least one cancer-associated Inhibitor of Apoptosis-
 CC family protein (IAP-family protein) and at least one immunoreactive gene
 CC product in a pharmaceutical carrier. The invention is useful for treating
 CC cancer such as lung cancer, colorectal cancer and melanoma. The present
 CC sequence is the human livin beta splice variant DNA.
 XX
 SQ Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;
 Alignment Scores:

Pred. No.: 3,646-257 Length: 1268
 Score: 280.00 Matches: 280
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 90.6% Indels: 0
 DB: 13 Gaps: 0

US-09-762-577B-12 (1-309) x AD571346 (1-1268)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
 Db 174 ATGGAGACCTTAAGACAG 233
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 Db 234 GCCGTGTATGTCTCCACCGAG 293
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
 Db 294 GAGCTGACACCTGACAG 353
 QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGln 413
 Db 354 CCCTGACAG 413
 QY 81 PheProGlyMetGlySerGlyGluLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
 Db 414 TTCCCGGACATGGGCTCTGAG 473
 QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 Db 474 GCTAGAGTGCACCCGAG 533
 QY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
 Db 534 AAGGTAGAGTGTCTTCTCTCTATGGGGGCTCTCAAGAGAGAGAGAGAGAGAGAGAGAG 593
 QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
 Db 594 TGACGAGAGATCCCAAGTGTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 653
 QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
 Db 654 GACTTGTCCACAGTGTGAG 713
 QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200
 Db 714 GAAGAACCGAG 773
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220
 Db 774 CTGCCACACCCAGAT 833
 QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnArgThrGlyValCysLeuAspArg 240
 Db 834 GTGAGAGGCGCAGCTCGCGCGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
 QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
 Db 894 GCCGTGTCATCGCTCTTGTCCTGCGCGCAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 953

RESULT 7
 ID AAF24856 standard; cDNA; 1376 BP.
 AC AAF24856;
 XX
 DT 20-APR-2001 (first entry)
 XX

DE Nucleotide sequence of an apoptosis inhibitor designated livin.
 XX
 XX Livin; apoptosis inhibitor; IAP-3; cancer; apoptosis; gene therapy;
 KW melanoma; Alzheimer's disease; Parkinson's disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 211..1053
 FT CDS /*tag= a
 FT /product= "livin"
 XX
 FN MO200077201-A1.
 XX
 PD 21-DEC-2000.
 XX
 XX 09-JUN-2000; 2000WO-GB002272.
 XX
 XX 15-JUN-1999; 99US-0139291P.
 XX
 XX (ASTR) ASTRAZENECA AB.
 XX (ASTR) ASTRAZENECA UK LTD.
 XX
 XX Gomes BC, Kasof GM, Prosser JC;
 XX
 XX MPI; 2001-122843/13.
 XX P-PSDB; AAB31478.
 XX
 XX Novel livin polypeptides and polynucleotides useful for treating
 PT pathophysiological disorders related to apoptosis; cancers, particularly
 PT melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene
 PT therapy.
 XX
 XX
 XX Claim 8; Page 53-54; 62pp; English.
 XX
 XX The present sequence encodes a human polypeptide, designated livin. Livin
 CC is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in
 CC certain cancer cell lines and prevents apoptosis. The livin polypeptide
 CC is useful for identifying compounds that inhibit and modulate livin
 CC function and activity. Such compounds are useful in the treatment of a
 CC dysfunctional apoptosis condition. Livin polypeptides are useful as a
 CC source of probes and primers, and in gene therapy. Livin polypeptides and
 CC polynucleotides, their inhibitors and modulators are useful for treating
 CC pathophysiological disorders related to apoptosis; cancers, particularly
 CC melanoma cancer, Alzheimer's disease and Parkinson's disease
 CC
 XX
 XX Sequence 1376 BP; 233 A; 432 C; 454 G; 257 T; 0 U; 0 Other;
 XX
 XX
 XX Alignment Scores:
 XX Pred. No.: 3.93e-257 Length: 1376
 XX Score: 280.00 Matches: 280
 XX Percent Similarity: 100.0% Conservative: 0
 XX Best Local Similarity: 100.0% Mismatches: 0
 XX Query Match: 90.6% Indels: 0
 XX DB: 4 Gaps: 0
 XX
 XX US-09-762-577B-12 (1-309) x AAF24856 (1-1376)
 XX
 QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
 Db 211 ATGGGACCTTAAGACAGTGCCTGCACTGACCCCTGACCAAGCCGACCTGGCA 270
 QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
 Db 271 GCCCGTATGTGTCACGACGACGCGCTGTGACCCCGCTCTGGGAGCCCTGTCTTA 330
 QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 Db 331 GGCCCTGGACCTGAGAGCTGGGACCACTGGATGGGCAATCTGGGCACTGGCGG 390
 QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGluGlnGlu 80
 Db 391 CCCCTGACAG 450

QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
 Db 451 TTCCCGGCGCATGGGCTCTGAGAGATTGCTGTGGCTCTTCTATGACTGGCCGCTACT 510
 QY 101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 Db 511 GCTAGGATGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570
 QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrPlyAspArgGlyAspAspPro 140
 Db 571 AAGGTGAGGTGCTTCTCTCTGCTATGGGGCTGTGAGAGCTGGAAGCCCGGGAGACAGCCC 630
 QY 141 TyrThrGlnHisAlaValTyrPheProSerCysGlnPheLeuLeuArgSerGlyArg 160
 Db 631 TGGACGAGGATGCAAGTGGTCCCGACGCTGTCAGTTCCTGCTCCGCTCAAAAGCAAGA 690
 QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
 Db 691 GACTTGTCCACAGTGTGACGAGACTCACTCCAGCTGTGGGCTCTGGAGCCGCTGG 750
 QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
 Db 751 GAGAAACCGGAAGACGACGCCCTGTGGCCCTCCCTCCCTGCTGTGGGTACCTGAG 810
 QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
 Db 811 CTGCCCAACCCAGAGAGAGAGTCCAGTCTGAAGTCCACAGAGCCAGAGCCAGAGGAT 870
 QY 221 ValGlnValGlnLeuArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
 Db 871 GTGAGGCGGAGCTGCGCGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
 QY 241 AlaValSerIleValPheValProCysGlyHisIleValCysAlaGlnCysAlaProGly 260
 Db 931 GCCGTGTCATGCTCTTGTGGCGCTGGCGGACCTGCTGTGTGCTGTGCTGTGCTGTGCT 990
 QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
 Db 991 CTCGAGCTGTGCCCATCTGCAGAGCCCGCTCGAGCGCGGCGGACCTTCTCTCTCC 1050
 XX
 XX RESULT 8
 XX AAL42857
 XX ID AAL42857 standard; DNA; 672 BP.
 XX
 XX AC AAL42857;
 XX
 XX DT 05-AUG-2002 (first entry)
 XX
 XX DE Survivin-like protein coding sequence 4.
 XX
 XX KW Survivin-like protein; diagnosis; screening; cancer; gene; ds;
 XX apoptosis abnormality; gene therapy.
 XX
 XX OS Unidentified.
 XX
 XX
 XX FH Key Location/Qualifiers
 XX FT 1..672
 XX FT CDS /*tag= a
 XX FT /partial
 XX FT /product= "Survivin-like protein 4"
 XX FT /note= "No stop codon is given"
 XX
 XX FN MO200233071-A1.
 XX
 XX PD 25-APR-2002.
 XX
 XX PF 16-OCT-2001; 2001WO-JP009071.
 XX
 XX XX 17-OCT-2000; 2000JP-00316721.
 XX PR 20-DEC-2000; 2000JP-00386809.
 XX
 XX PA (TAKE) TAKEDA CHEM IND LTD.

XX Tanaka H, Kaieda I;
 XX WPI; 2002-435536/46.
 DR P-PSDB; AAO14946.
 XX
 XX Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
 PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
 PT compounds for treating various cancers and apoptosis abnormality.
 XX
 PS Claim 85; Page 119-120; 136pp; Japanese.
 CC The invention comprises the amino acid and coding sequences of survivin-
 CC like proteins. The survivin-like DNA and protein sequences are useful in
 CC diagnostics and screening compounds for treating various cancers and
 CC apoptosis abnormality, including gene therapy. The present DNA sequence
 CC encodes a survivin-like protein of the invention
 XX
 SQ Sequence 672 BP; 116 A; 216 C; 228 G; 111 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	2.96e-198	Length:	672
Score:	218.00	Matches:	218
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	70.6%	Indels:	0
DB:	6	Gaps:	0

US-09-762-577B-12 (1-309) x AAL42857 (1-672)

QY 1 MetGlyProlyAspSerAlaIysCySLeuHisArgGlyProGlnProSerHisTrpAla 20
 Db 1 ATGGGGCTTAAGACAGTGCACAGTCCCTGCACCGTGCACACAGCCGACCTGGGCA 60
 QY 21 AlaGlyAspGlyProThrGlnGluArgCySgLyProArgSerLeuGlySerProValLeu 40
 Db 61 GCCGGTGAATGGTCCACGAGGAGCGCTGTGGACCCCGCTCTGTGGGAGCCCTGCTTA 120
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
 Db 121 GGCTTGGACACCTGGACAGCCTGGGACCGTGGATGGGACAATCTGGGCGACGTCGG 180
 QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 Db 181 CCCCTGACAG 240
 QY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyAspTrpProLeuThr 100
 Db 241 TTCCTCCGCAATGGCTCTGAAGAGTGGCTGTGGCTCTCTTATGACTGGCGCTGACT 300
 QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
 Db 301 GCTGAGGTGCCACCCGACGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 360
 QY 121 LysValArgCysPhePheCysTyArgIlyLeuGlnInserrTrpLysArgGlyAspAspPro 140
 Db 361 AAGGTGAAGTGTCTTCTGTCTATGAGGGCTGTGACAGAGTGAAGCGGGGACACACCC 420
 QY 141 TrpThrGlnHisAlaIySerTrpPheProSerCysGlnPheLeuLeuArgSerIlyArg 160
 Db 421 TGGAGCGAGCATGCCAAGTGTCTCCCACTGTCACTGTCTGTCTGTCTGTCTGTCTGT 480
 QY 161 AspPheValHisSerValGlnGlnIleThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
 Db 481 GACTTTGTTCACAGTGTGACAGAGACTCACTCCAGCTGTGGCTGTGGAGCCCGTGG 540
 QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyPProGlu 200
 Db 541 GAAAGAACCGAAGACAGCCCTGTGTGGCCCTCTGTCTGTGGTGTACCTGTAG 600
 QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyValA 218
 Db 601 CTGCCACACCCACGAGAGAGAGTCCAGTCTGAAATGCTCCAGAGACCGAGTCCA 654

RESULT 9

AAL42856
 ID AAL42856 standard; DNA; 723 BP.

XX AAL42856;

XX 05-AUG-2002 (first entry)

XX Survivin-like protein coding sequence 3.

XX
 XX Survivin-like protein; diagnosis; screening; cancer; gene; ds;
 XX apoptosis abnormality; gene therapy.
 XX
 OS Unidentified.

XX Key Location/Qualifiers
 FT CDS 1..723
 FT /*tag=a
 FT /partial
 FT /product="Survivin-like protein 3"
 FT /note="No stop codon is given"

XX WO200233071-A1.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-JP009071.

XX 17-OCT-2000; 2000JP-00316721.

XX 20-DEC-2000; 2000JP-00386809.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Tanaka H, Kaieda I;

XX WPI; 2002-435536/46.

XX P-PSDB; AAO14945.

XX
 XX Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
 PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
 PT compounds for treating various cancers and apoptosis abnormality.
 XX
 PS Claim 5; Page 117-118; 136pp; Japanese.

CC The invention comprises the amino acid and coding sequences of survivin-
 CC like proteins. The survivin-like DNA and protein sequences are useful in
 CC diagnostics and screening compounds for treating various cancers and
 CC apoptosis abnormality, including gene therapy. The present DNA sequence
 CC encodes a survivin-like protein of the invention
 XX

SQ Sequence 723 BP; 123 A; 230 C; 252 G; 117 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	3.16e-198	Length:	723
Score:	218.00	Matches:	218
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	70.6%	Indels:	0
DB:	6	Gaps:	0

US-09-762-577B-12 (1-309) x AAL42856 (1-723)

QY 1 MetGlyProlyAspSerAlaIysCySLeuHisArgGlyProGlnProSerHisTrpAla 20
 Db 1 ATGGGGCTTAAGACAGTGCACAGTCCCTGCACCGTGCACACAGCCGACCTGGGCA 60
 QY 21 AlaGlyAspGlyProThrGlnGluArgCySgLyProArgSerLeuGlySerProValLeu 40
 Db 61 GCCGGTGAATGGTCCACGAGGAGCGCTGTGGACCCCGCTCTGTGGGAGCCCTGCTTA 120
 QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60

[illegible]

RESULT 10	
ADH89543	
ID	ADH89543 standard; DNA; 1168 BP.
XX	
AC	ADH89543;
XX	
DT	22-APR-2004 (first entry)
XX	
DE	Human Livin genomic DNA #2.
XX	
KW	hyperproliferative disorder; aberrant apoptosis; human; ds; livin; gene
XX	
OS	Homo sapiens.
XX	
PN	US2004005565-A1.
XX	
PD	08-JAN-2004.
XX	
PF	02-JUL-2002; 2002US-00188646.
XX	
PR	02-JUL-2002; 2002US-00188646.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
P1	Bennett CF, Dobie KW;
XX	
DR	WPI; 2004-098436/10.
XX	
DR	P-PSDB; ADH89686.
XX	
PT	New antisense oligonucleotide, having a sequence targeted to a nucleic
PT	acid encoding Livin, useful for preparing a composition for treating
PT	hyperproliferative disorder or aberrant apoptosis.
XX	
PS	Example 15; SEQ ID NO 12; 60pp; English.
XX	
CC	The invention relates to an antisense oligonucleotide targeted to a
CC	nucleic acid encoding Livin and that specifically hybridises with the
CC	nucleic acid encoding Livin and inhibits expression of Livin. The
CC	antisense oligonucleotide is useful for preparing a composition for

CC	treating hyperproliferative disorder or aberrant apoptosis. The present
CC	sequence represents human livin DNA.
XX	
XX	Sequence 1168 BP, 206 A, 357 C, 393 G, 212 T, 0 U, 0 Other;
Alignment Scores:	
Pred. No.:	4.42e-197
Score:	217.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	70.2%
DB:	12
	Gaps: 0
	Length: 1168
	Matches: 217
	Conservative: 0
	Mismatch: 0
	Indels: 0
	Gaps: 0

US-09-762-577B-12 (1-309) x ADH89543 (1-1168)

OY	1	MetG1ProLYaSPbSbzrAlaLYsCYsLueH1sarGQ1YProG1nProSeH1sTryAla	20
Db	1	ATGGAGCCTTAAGACAGTGCATGTCCCTGCACCCGGACACACCCGACCTCGGGCA	60
OY	21	AlaG1YAaSPg1YProThrg1ng1uArCYsG1YProArGserLueG1YSerProValLeu	40
Db	61	GCCCGTATGATGCCACGACGAGGCGCCTGTGGACCCCTCTCTGGCAGCCCTGTCTTA	120
OY	41	G1YLeuAspThrCYsarG1a1aTrPaSPH1sValaSPg1Yg1n1eLueG1Yg1LeuArg	60
Db	121	GGCTTGACACCTGCGAGCGCTGGACACACGTGGATGGGACAGATCTGTGGCCCACTGGG	180
OY	61	ProLeuThrG1uG1uG1uG1uG1uG1YAlaG1YAlaThrLeuSerHArgG1YProAla	80
Db	181	CCCTGTGACAGGAGAAAGAGAGAGGGCGCGCGGACCTTGTCCAGGGGGCCCTGGC	240
OY	81	PheProG1YMetG1YserG1uG1uLeuAArgLeuAlaSerPheYrAspTrpProLeuThr	100

[illegible]

RESULT 11	
ACC72843	
ID	ACC72843 standard; cDNA; 1322 BP.
XX	
XX	
AC	ACC72843;
XX	
DT	09-JUL-2003 (first entry)
XX	
DE	Human cancer related protein encoding cDNA SEQ ID NO:181.
XX	
KW	Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia
KW	heart disease; atherosclerosis; gene; ss.
XX	
OS	Homo sapiens.

PT response against cancer.

XX Claim 26, SEQ ID NO 26; 84pp; English.

CC The present invention relates to a DNA vaccine effective for eliciting an
CC immune response against cancer cells which comprises a DNA construct
CC operably encoding at least one cancer-associated inhibitor of apoptosis-
CC family protein (IAP-family protein) and at least one immunosuppressive
CC product in a pharmaceutical carrier. The invention is useful for treating
CC cancer such as lung cancer, colorectal cancer and melanoma. The present
CC sequence is the human livin alpha splice variant DNA.

XX Sequence 1322 BP; 212 A; 417 C; 445 G; 248 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,96e-197	Length:	1322
Score:	217.00	Matches:	217
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	70.2%	Indels:	0
DB:	13	Gaps:	0

US-09-762-577B-12 (1-309) x AD871344 (1-1322)

```

OY 1 MetGlyProlyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 174 ATGGAGCTTAAGACAGTGCAGAGTCTGCACCGTGGACACAGCCAGCCACTGGGCA 233
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 234 GCCGATATGCTCCACCCAGAGAGCGCTGTGAGACCCCGCTCTGTGGAGAGCCCTGTCTTA 293
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 294 GGCTTGACACCTCCAGAGAGCTGGGACCACTGATGGGACAGATCTGTGGCCAGCTGGG 353
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 354 CCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
OY 81 PheProGlyMetGlySerGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
DB 414 TTCCCGGCGAGGCTCTGAGAGAGTGTGGCTGTGGCTCTCTTGTAGCTGAGCCCTGACT 473
OY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 474 GCTGAGGTGCCACCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
OY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 534 AAGGTGAGGTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 593
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 594 TGGAGGAGGAGTGCAGAGTGTCTCCACAGCTGTCAAGTTCCTGCTCCGCTCAAAAGAGA 653
OY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 654 GACTTTGTCCACAGTGTGCAGAGAGCTCAGCTCCAGAGTGTGGGCTCTTGGGAGCCCGT 713
OY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
DB 714 GAAGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773
OY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlnGlnGlnGlnGln 217
DB 774 CTGCGCACACCCAGAGAGAGAGTCCAGTCTAAAGTCCCGAGAGAGAGAGAGAGAGAG 824

```

RESULT 13

AAZ61210 ID AAZ61210 standard; DNA; 1337 BP.
XX AC AAZ61210;

```

XX 30-MAY-2000 (first entry)
DT DNA encoding a human inhibitor of apoptosis protein (HIAP3).
XX
DE Human; inhibitor of apoptosis protein; HIAP3; apoptosis; cancer;
XX chronic viral infection; neurodegenerative disorder;
XX chronic heart failure; dysfunctional immune response; sg.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 170..1066
FT /tag= a
FT /product= "human inhibitor of apoptosis protein"
XX
XX MO200008144-A1.
XX
XX 17-FEB-2000.
XX
XX 23-JUL-1999; 99WO-EP005471.
XX
XX 31-JUL-1998; 98US-00127928.
XX
XX (SCHD ) SCHERING AG.
XX
XX Deng G, Lin J, Morser MJ;
XX
XX WPI: 2000-195573/17.
XX DR P-PSDB; AA66182.
XX
XX New DNA encoding human inhibitor-of-apoptosis protein, useful for
XX regulation of apoptosis.
XX
XX Claim 10; Fig 1, 57pp; English.
XX
XX The present sequence encodes a human inhibitor of apoptosis protein,
XX designated HIAP3. The protein is characterised by structural features
XX common to the inhibitor of apoptosis protein family. The HIAP3
XX polypeptides can be used for the treatment of a disease state in a human
XX patient, which is associated with inappropriate apoptosis and the patient
XX is in need of increased levels of the polypeptide. Ribozymes, which
XX target RNA encoding the polypeptide coding sequences, are useful for
XX decreasing levels of the polypeptide for treatment of inappropriate
XX apoptosis. Antisense nucleotide sequences are also useful for decreasing
XX levels of the polypeptide. Regulation of inhibitor of apoptosis proteins
XX may be useful in treatment of cancer, chronic viral infections,
XX neurodegenerative disorders, chronic heart failure and dysfunctional
XX immune response
XX
XX
XX Sequence 1337 BP; 231 A; 413 C; 445 G; 248 T; 0 U; 0 Other;
SQ

```

Alignment Scores:

Pred. No.:	5.01e-197	Length:	1337
Score:	217.00	Matches:	217
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	70.2%	Indels:	0
DB:	3	Gaps:	0

US-09-762-577B-12 (1-309) x AAZ61210 (1-1337)

```

OY 1 MetGlyProlyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 170 ATGGAGCTTAAGACAGTGCAGAGTCTGCACCGTGGACACAGCCAGCCACTGGGCA 229
OY 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
DB 230 GCCGATATGCTCCACCCAGAGAGCGCTGTGAGACCCCGCTCTGTGGAGAGCCCTGTCTTA 289
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 290 GGCTTGACACCTCCAGAGAGCTGAGACCACTGATGGGACAGATCTGTGGCCAGCTGGG 349

```

OY	61	ProLeuthrGluGluGluGluGluGluGluGluValAGlyAlaThrLeuSerArgIleProAla	80
Db	350	CCCCGTGCAGAGGAGGAAGAGAGGGGGCCGGGGCCACTTCTGCCAGGGGGCTGCC	409
OY	81	PheProGlyMetCysGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuthr	100
Db	410	TTCGCCGGCATGGGCTCTGAGGAGATTGGCTTGCGCTCTTTATGACCTGGCGGTGACT	465
OY	101	AlaGluValProproGluLeuLeuAlaAlaAlaGlyPhePheIstHrgIyHISGlnASP	120
Db	470	GCTAAGGTGCACCCTGCAGCTGCTGCCTGCCGGCTTCTTCCACACAGGCCATCACAGAC	529
OY	121	LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgIleAspAspPro	140
Db	530	AAGGTGAGGTGCTCTCTTCTGCTATGGGGGCTGCAGAAGTGGAAAGCGGGGAGACCCC	589
OY	141	TrpThrGluHisAlaAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg	160
Db	590	TGGACGGAGCATCCCAAGTGGTCCCCACCATCTCAGTTCCTGCTCCGGTCAAAGAGACA	649
OY	161	AspPheValHisSerValGlnGluTrpHisSerGlnLeuLeuGlySerTrpAspProTrp	180
Db	650	GACTTTGTCCACAGGTGTGCAGAGACTCACTCCACAGCTGCTGGGCTCTTGGAACCCCTGG	709
OY	181	GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu	200
Db	710	GAAAGAACCGGAMAACCCACGCCCTGTGGGCCCTCCGCTCCGTCTGGGGTNACCTGAG	769
OY	201	IleProThrProArgArgGluValGlnSerGlySerAlaGlnGluProGly	217
Db	770	CTCCCCACACCCAGGAGAGAGTCCAGTCTGAAGATGGCCACGAGGCCAGAGA	820

RESULT 14
AAA15007
ID AAA15007 standard; cDNA; 1363 BP.

AC AAA15007;

DT 21-AUG-20

first entry)

CDNA encoding a human proliferation and apoptosis related protein.

KM Human; proliferation and apoptosis related protein; PROAP; psoriasis;
KM cell proliferative disorder; immunological disorder; hepatitis;
KM reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma;
KM cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia;
KM asthma; diabetes mellitus; osteoarthritis; endometriosis;
KM uterine fibroid; menstrual cycle; ss.

OS Homo sapiens.

FH ET	Key and	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

```

FT      420.1111
FT      /*tag= a
FT      /product= "proliferation and apoptosis related protein"

```

PN WO2000023589-A2

PD 27-APR-2000.

PF 19-OCT-1999; 99WO-US024511.
VV

PR 20-OCT-1998; 98US-0172216P.
 DP 04-FEB-1999; 98US-0172216P.

PR	11-FEB-1999;	99US-0172229P.
PR	22-APR-1999.	99US-0172229P.

XX
PA (INCY-) INCYTE PHARM INC

XX
PI Tang YT, Yue H, Hillman JL, Guegler KJ, Corley NC, Lal P;
PI Azimzai Y, Baughn MR, Yang J, Shih LL;
XY

DR WPI; 2000-339688/29.
DR P-PSDB; AAY84907.

DR P-PSDB; AAY84907.

PT New human proliferation and apoptosis related protein polypeptides used
PT for diagnosis, treatment and prevention of cell proliferative,
PT immunological and reproductive disorders.

Claim 9; Page 121; 128pp; English.

The present sequence encodes a human proliferation and apoptosis related protein (PROAP). The polypeptides and polynucleotides can be used for the diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders. Disorders associated with decreased expression or activity of include arteriosclerosis, cirrhosis, hepatitis, psoriasis, melanoma, lymphoma and cancers of the breast, brain and prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemia, asthma, diabetes mellitus, osteoarthritis, endometriosis, uterine fibroids and disruptions of the menstrual cycle. Antibodies against PROAP can be used in diagnosis of disorders characterized by PROAP e.g. in ELISA (enzyme linked immunosorbent assays) and the polynucleotides may be used to detect and quantify gene expression in biopsied tissues. These techniques can also be used to monitor regulation of PROAP levels during therapeutic intervention.

SQ Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.1e-197	Length:	1363
Score:	217.00	Matches:	217

Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%		

```

Query Match: 70.2%
Mismatches: 0
Indels: 0

```

DB: 3
Gebruik: 0

US-09-762-577B-12 (1-309) x AAA15007 (1-1363)

QY 1 MetGlyPProLysASPSPeRAAlaLysCysLeuHisArgGlyProGlnProSerHisTyrPala 20

Db 215 ATGGGGCTAAGACAGTGCCTGCACCGTGGACCAAGCCGAGCCACTGGCA 274

21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40

2 / 3 G C C G G A G A G C C T G T G G G C A G C C C T G T C C T A 334

...cysnsp...icysaligladilpraphtisvalabpsllyglnlleleuglyglnleuarg 60

[illegible][illegible]

81 Phosphorylation of the α -subunit of the Ca^{2+} pump

455

[illegible]

D**b**

515 GCTGAGGTGCCACCCGAGCTGCTGAGCTGACCGACTTCTTTCAACAAGCACAATCAAGCAC 674

121 LysValArgCysPhePheCysTyrGlvGlVLeuGlnserTrpLysArgGlvAsnAsnPro 140

Db 575 AAGTGAGTCTTCTTCTGCTATGGGGCCTGCAGAGCTGGAAGCGGGGACGACCC 634

QY 141 TrpThrGluHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160

Db 635 TGGACGGAGCATGCCAAGTGGTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAGA 694

161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTyr 180

Db 695 GACTTGTCCACAGTGTGCAGGAGCTCACTCCACGCTGTGGCTCCTGGACCCGTGG 754

DB 755 GAAAGACCGAGAGACGACCCCTGTGCCCCCTCCCTGCTGAGTACCCCTGAG 814
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
DB 815 CTGCCACACCCAGAGAGAGGTCCAGTCTGAAGTGGCCAGACCGACGGA 865

RESULT 15
ADT88075
ID ADT88075 standard; cDNA; 1363 BP.
AC ADT88075;
XX
XX
DT 30-DEC-2004 (first entry)
XX
DE Human proliferation and apoptosis related protein (PROAP)-18 cDNA.
XX
XX
KW PROAP; proliferation and apoptosis related protein;
KW cell proliferative disorder; cancer; atherosclerosis;
KW immunological disorder; AIDS; acquired immunodeficiency syndrome;
KW allergy; reproductive disorder; infertility; gene therapy; cytostatic;
KW antiatherosclerotic; immunosuppressive; anti-HIV; antiallergic;
KW antiinfertility; gynaecological; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 215..1111
FT /tag= a
FT /product= "Proliferation and apoptosis related protein
FT (PROAP)-18"
XX
XX
XX US2004203106-A1.
XX
XX PD 14-OCT-2004.
XX
XX PF 05-MAY-2004; 2004US-00839882.
XX
XX PR 19-JAN-1999; 99US-0172216P.
XX PR 04-FEB-1999; 99US-0118559P.
XX PR 11-FEB-1999; 99US-0172229P.
XX PR 22-APR-1999; 99US-0154336P.
XX PR 19-OCT-1999; 99MO-US024511.
XX PR 11-APR-2001; 2001US-00807452.
XX
XX PA (INCY-) INCYTE CORP.
XX
XX PI Tang YT, Yue H, Hillman JL, Guegler KJ, Corley NC, Lal P;
XX PI Azimzai Y, Baughn MR, Yang J, Shin LL;
XX
XX DR WPI; 2004-728011/71.
XX DR P-PSDB; ADT88056.
XX
XX PT New human proliferation and apoptosis related proteins and
XX PT polynucleotides for diagnosing, preventing or treating disorders
XX PT associated with aberrant protein expression, e.g. cancer, AIDS,
XX PT atherosclerosis or infertility.
XX
XX PS Claim 5; SEQ ID NO 37; 85pp; English.
XX
XX CC The present invention relates to the human proliferation and apoptosis
XX CC related protein (PROAP) and its encoding nucleic acid. The invention is
XX CC useful for diagnosing, preventing or treating disorders associated with
XX CC altered expression or activity of human PROAP, such as cell proliferative
XX CC (e.g. cancer or atherosclerosis), immunological (e.g. acquired
XX CC immunodeficiency syndrome (AIDS) or allergies) or reproductive (e.g.
XX CC infertility) disorders. The invention is also used in screening for
XX CC drugs that may be used for treating or preventing the disorders mentioned
XX CC above and in gene therapy. The present sequence is the human PROAP-18
XX CC protein encoding cDNA.
XX
XX SQ Sequence 1363 BP; 228 A; 428 C; 455 G; 252 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,1e-197 Length: 1363
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
DB: 13 Gaps: 0

US-09-762-577b-12 (1-309) x ADT88075 (1-1363)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 215 ATGGGGCTTAAGACAGTGCACAGTGCCTGCACCTGACACACAGCCGACCATGGGCA 274
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 275 GCCGATAGTGTCCACAGCAGAGACGGCTGTGAGACCCGCTCTCTGGGACAGCCCTGTCTTA 334
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
DB 335 GGCTTGACACCTGACAGAGCTGGGACCATGTGATGGGAGATCTTGGGCGACCTGGG 394
QY 61 ProLeuThrGlnGlnGluGlnGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 395 CCCCTGACAG 454
QY 81 PheProGlyMetGlySerGlnGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 455 TTCCCGGCAATGGGCTCTGAGAGAGTTCGCTGTGCTCTCTCTGATGACTGGCGCTGACT 514
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 515 GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 575 AAGGTGAGTGTCTTCTCTGCTATGGGGGCTTGCAGAGCTTGGAGCCGGGGAGACCC 634
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 635 TGAACGAGCATGTCAGATGGTTCCTCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGAGA 694
QY 161 AspPheValHisSerValGlnGluTrpHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 695 GACTTGTCCACAGCTGTCAGAGAGACACCTCCAGCTGCTGGGCTCTCTGGGACCCGTGG 754
QY 181 GluGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 755 GAAAGACCGAG 814
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
DB 815 CTGCCACACCCAGAGAGAGGTCCAGTCTGAAGTGGCCAGACCGACGGA 865

Search completed: April 24, 2006, 11:11:43
Job time : 742 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2006, 09:59:36 ; Search time 4508 Seconds

(without alignments)

3207.012 Million cell updates/sec

Title: US-09-762-577B-12

Perfect score: 309

Sequence: 1.MGPKDSAKCLHRGPQPSHMA.....GLQSLPAPLCIFMTVFWAC 309

Ygapop 60.0 , Ygapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82154962

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-Q=/abs/ABSSMB.spool/US09762577/runat_24042006_105924_898/app.query.fasta_1
-DB=EST -QFMT=fastcap -SUFFIX=p2noli.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -
-UNITS=bite -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco
-NORR=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs802h
-USER=US09762577.QCGN_1_1_5315_@runat_24042006_105924_898 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DISPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hrc: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss1: *
10: gb_gss2: *
11: gb_gss3: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	217	70.2	884	5 BUI95879
2	217	70.2	924	5 BUI95879
3	210	68.0	982	5 B0682827
4	206	66.7	621	6 B0682897
5	205	66.3	945	5 B0673774
6	204	66.0	929	5 BUI80020
7	192	62.1	918	5 B0892691
				5 BUI50825

8	187	60.5	740	2 B0768992	B0768992	602742820
9	187	60.5	877	2 B0770075	B0770075	602745008
10	185	59.9	956	5 BUI68025	BUI68025	AGENCOURT
11	181	58.6	956	5 BUI72109	BUI72109	AGENCOURT
12	181	58.6	958	5 BUI88703	BUI88703	AGENCOURT
13	180	58.3	603	3 B0696272	B0696272	UI-E-DW0-
14	176	57.0	870	5 B0877438	B0877438	AGENCOURT
15	176	57.0	912	5 B0682378	B0682378	AGENCOURT
16	176	57.0	919	5 B0877652	B0877652	AGENCOURT
17	175	56.6	555	2 B0726384	B0726384	by05h02.y
18	172	55.7	616	2 B0767481	B0767481	602741287
19	171	55.3	920	5 B0676590	B0676590	AGENCOURT
20	167	54.0	830	2 B0762467	B0762467	602733911
21	160	51.8	652	2 B0763730	B0763730	602735757
22	157	50.8	824	2 B0770578	B0770578	602734106
23	154	49.8	623	3 B0700577	B0700577	UI-E-DW1-
24	147	47.6	506	5 B0283097	B0283097	BX283097
25	146	47.2	579	6 CD673799	CD673799	60273799
26	145	46.9	952	5 B0678815	B0678815	AGENCOURT
27	143	46.3	655	2 B0760550	B0760550	602716990
28	140	45.3	797	2 B0766472	B0766472	602739233
29	140	45.3	849	2 B0760865	B0760865	602717048
30	140	45.3	902	5 BUI83453	BUI83453	AGENCOURT
31	137	44.3	808	2 B0761924	B0761924	602718156
32	131	42.4	665	3 B0704611	B0704611	UI-E-C11-
33	128	41.4	570	2 B0727035	B0727035	by15h01.y
34	123	39.8	371	3 B0717934	B0717934	UI-E-EJ0-
35	121	39.2	668	5 B0679311	B0679311	AGENCOURT
36	119	38.5	633	5 B0742147	B0742147	UI-E-EJ0-
37	118	38.2	999	5 BUI94400	BUI94400	AGENCOURT
38	116	37.5	843	11 D0053047	D0053047	Homo sapi
39	101	32.7	497	6 CB113932	CB113932	K-EST0157
40	101	32.7	843	2 B0770473	B0770473	602734384
41	99	32.0	843	2 B0766949	B0766949	602740652
42	99	32.0	1248	5 B0679638	B0679638	AGENCOURT
43	95	30.7	891	6 CD051153	CD051153	AGENCOURT
44	87	28.2	741	2 B0763960	B0763960	602736948
45	80	25.9	303	5 B0681718	B0681718	AGENCOURT

ALIGNMENTS

RESULT 1
BUI95879
LOCUS
DEFINITION
AGENCOURT 8050326 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089315
5', mRNA sequence.
ACCESSION
BUI95879
VERSION
BUI95879.1 GI:22709863
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo
1 (bases 1 to 884)
REFERENCE
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LINCW328 row: 0 column: 12
High quality sequence stop: 658.
Location/Qualifiers
1..884
/organism="Homo sapiens"

FEATURES

source

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6089315"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB1; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ALIGNMENT SCORES:

Pred. No.: 9.24e-198 Length: 884
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
DB: 5 Gaps: 0

US-09-762-577B-12 (1-309) x BUI95879 (1-884)

```
QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 64 ATGGAGCCTTAAAGACAGTGCCTGCTGACCTGAGACACAGCCGAGCAGCTGGGCA 123
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 124 GCGGTGATGATGCCAGCAGGAGCGCTGGACCCCGCTCTGGGAGCCCTGTCCCTA 183
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 184 GGCCTGGACACCTGCGAGAGCTTGGACACAGTGGATGGCAATCTGGGCGAGCTGGCG 243
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 244 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
DB 304 TTCCCGGCAATGGGCTCTGAGAGATTGCGTGGCCCTCTTATGACTGGCCGCTGACT 363
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 364 GCTGAGGTGCACCCGAGCGTGGCTGCTGCGGCTTCTTCCACACAGGCCATCAGGAC 423
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 424 AAGGTAGAGTCTTCTTCTGCTAATGGGGCCCTGACAGAGCTGGAACGCGGGAGCAGCCC 483
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 484 TGGACGAGACATGCCAAGTGTTCCTCCAGCTTCACTGCTGCTCGGTCAAAAGAGAA 543
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
DB 544 GACTTGTTCACAGTGTGACAGAGACTCCTCCAGCTGCTGGGCTCTTGGAGCCCGTGG 603
QY 181 GlnGlnProGlnLysAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
DB 604 GAAAGAACCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnGlnGlnGlnGln 217
DB 664 CTGCCACACACCCAGAGAGAGAGTCCAGTCTGAAGTCCCGCCAGAGCCAGAGA 714
```

RESULT 2
BO682827
LOCUS

BO682827 924 bp mRNA linear EST 15-JUL-2002

DEFINITION AGCNCOURT 8507903 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6294748
5', mRNA sequence.
ACCESSION BO682827
VERSION BO682827.1 GI:21795506
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
REFERENCE 1 (bases 1 to 924)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LICM2499 row: 0 column: 05
High quality sequence, stop: 673.

FEATURES

source

1..924
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6294748"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB1; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

ALIGNMENT SCORES:

Pred. No.: 9.64e-198 Length: 924
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
DB: 5 Gaps: 0

US-09-762-577B-12 (1-309) x BO682827 (1-924)

```
QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 64 ATGGAGCCTTAAAGACAGTGCCTGCTGACCTGAGACACAGCCGAGCAGCTGGGCA 123
QY 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
DB 124 GCGGTGATGATGCCAGCAGGAGCGCTGGACCCCGCTCTGGGAGCCCTGTCCCTA 183
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 184 GGCCTGGACACCTGCGAGAGCTTGGACACAGTGGATGGCAATCTGGGCGAGCTGGCG 243
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 244 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
QY 81 PheProGlyMetGlySerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
DB 304 TTCCCGGCAATGGGCTCTGAGAGATTGCGTGGCCCTCTTATGACTGGCCGCTGACT 363
```


PUBMED
COMMENT

12107413
Contact: Mielow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graham@helix.nih.gov
Plate: 04 row: C column: 01
Seq primer: M13RPL reverse primer (AB1).
Location/Qualifiers

FEATURES
source

1. .621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="f604c01"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Lens cDNA (Normalized): fs"
/note="Organ: Eye; Vector: pCMVSPORT6; A human lens library (by) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (COT 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/RNA-synthesized removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:

Pred. No.: 2,5e-187 Length: 621
Score: 206.00 Matches: 206
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 66.7% Indels: 0
DB: Gaps: 0

US-09-762-577B-12 (1-309) x CD673774 (1-621)

QY 8 LysCysLeuHisArgGlyProGlnProSerHisTTPAAlaGlyAspGlyProThrGln 27
Db 3 AAGTGGCTGGACCGTGGACCAAGCCGAGCCACTGGGACGCGGTGATGGTCCACGAG 62
QY 28 GluArgCysGlyProArgSerLeuGlySerProValLeuGlyLeuAspThrCysArgAla 47
Db 63 GAGCGGTGGACCCCGCTCTGGGGACCCCTGCTCTTACGGCTGGACACCTGGACAGACC 122
QY 48 TrpAspHisValAspGlyGlnLeuGlyGlnLeuArgProLeuThrGluGluGlu 67
Db 123 TGGGACCACTGGATGGGAGATCCGTGGGCCAGCTGGGCCCTTACAGAGAGAGAGAG 182
QY 68 GluGluGlyAlaGlyAlaThrLeuSerArgGlyProAlaPheProGlyMetGlySerGlu 87
Db 183 GAGGAGGGGGCGGGGGCCACTTGTCCAGGGGGGCTGCTCCCGGATGGGCTCTTACG 242
QY 88 GluLeuArgLeuAlaSerPheTyrAspTTPProLeuThrAlaGluValProProGluLeu 107
Db 243 GAGTGGCTGGCTGCTCTTATAGCTGGCCGCTGAGCTGGAGTGCACCCGAGCTG 302
QY 108 LeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAspLysValArgCysPhePhe 127
Db 303 CTGGGCTGGCGGGCTTCTTCCACAGGCCATTCAGGACAGAGTGAAGTGTCTTCTTGC 362
QY 128 TyrGlyGlyLeuGlnSerTTPLysArgGlyAspAspProTTPThrGluHisAlaLysTTP 147
Db 363 TATGGGGGCTTCAAGAGCTGGAAAGCGGGGAGCAGACCCCTGAGAGGAGCATGCCAAGTGG 422

QY 148 PheProSerCysGlnPheLeuLeuArgSerTyrArgAspPheValHisSerValGln 167
Db 423 TTCCCAAGCTGCACTTCTCTCCGGTCAAAAGGAAGACTTGTCCACAGCTGCAG 482
QY 168 GluThrHisSerGlnLeuGlySerTrpAspProTTPGluGluProGluAspAla 187
Db 483 GAGACTCACTCCAGCTGCTGGGCTCCCTGGGACCCGTGGAGAAACCGAAGACCGAGCC 542
QY 188 ProValAlaProSerValProAlaSerGlyTyrProGluLeuProThrProArgGlu 207
Db 543 CCTGTGGCCCCCTCGTCCCTGCTGTGGGATCCTTGAAGTGCACACCGAGAGAGAG 602
QY 208 ValGlnSerGluSerAla 213
Db 603 GTCCAGCTGTAAGTGC 620

RESULT 5
BU180020
LOCUS
DEFINITION
AGNCOURT 8106750 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6253787
5', mRNA sequence.
ACCESSION
BU180020
VERSION
BU180020.1 GI:22694004
KEYWORDS
EST.
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE
1 (bases 1 to 945)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strauberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LHC2402 row: d column: 12
High quality sequence start: 13
High quality sequence stop: 667.
Location/Qualifiers

FEATURES

source

1. .945
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6253787"
/tissue_type="melanotic melanoma, cell line"
/lab_host="NIH MGC 112"
/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGACAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3.41e-186 Length: 945
Score: 205.00 Matches: 205
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 66.3% Indels: 0
DB: Gaps: 0

US-09-762-577b-12 (1-309) x BUI80020 (1-945)

```
QY      1 MetGlyProlyAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db      90 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCTGTGACACACAGCCAGCCACTGGGACA 149
QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      150 GCCGTGATGGTCCACCGACGAGGCGCTGTGACCCCTCTCTGGGAGCCCTGTCTCTA 209
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      210 GGCTCGACACCTGTGAGAGCTGGGACCACTGATGGATGGAGATCTTGGCCAGCTGGCG 269
QY      61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      270 CCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329
QY      81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
Db      330 TTCCCGGCAATGGCTCTGAGAGATTGGCTGCTGCTCTCTCTATGACTGGCCGCTGACT 389
QY      101 AlaGluValProProGlnLeuLeuAlaAlaIaGlyPhePheHisThrGlyHisGlnAsp 120
Db      390 GCTGAGTGCCACCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      450 AAGGTGAGTGCTCTCTCTCTGCTATGGGGGCTGACAGACTGGAAGCGGGGAGACACCC 509
QY      141 TrpThrGlnHisAlaIysTrpPheProSerCysGlnPheLeuLeuAlaArgSerLysGly 160
Db      510 TGGACGGAGCATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
QY      161 AspPheValHisSerValGlnGlnIleThrHisSerGlnLeuGlnGlySerTrpAspProTrp 180
Db      570 GACTTTGTCCACAGTGTCCAGAGACTCACTCCAGCTGCTGGGCTCTGGGACCCGCTGG 629
QY      181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db      630 GAAGAACCGGAAGACGACAGCCCTGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 689
QY      201 LeuProThrProArg 205
Db      690 CTGCCACACCCAGA 704
```

RESULT 6
BOB92691 929 bp mRNA linear EST 16-AUG-2002
LOCUS BOB92691
DEFINITION AGNCOURT 8095843 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6087832
5', mRNA sequence.
ACCESSION BOB92691
VERSION BOB92691.1 GI:22284705
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsabbs-rc@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LNCM2325 row: a column: 17

High quality sequence stop: 628.

FEATURES

source

Location/Qualifiers

1..929

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6087832"

/tissue_type="melanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3,07e-185 Length: 929

Score: 204.00 Matches: 204

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 66.0% Indels: 0

DB: 5 Gaps: 0

US-09-762-577b-12 (1-309) x BOB92691 (1-929)

```
QY      1 MetGlyProlyAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db      90 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCTGTGACACACAGCCAGCCACTGGGACA 149
QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      150 GCCGTGATGGTCCACCGACGAGGCGCTGTGACCCCTCTCTGGGAGCCCTGTCTCTA 209
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      210 GGCTCGACACCTGTGAGAGCTGGGACCACTGATGGATGGAGATCTTGGCCAGCTGGCG 269
QY      61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      270 CCCCTGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329
QY      81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
Db      330 TTCCCGGCAATGGCTCTGAGAGATTGGCTGCTGCTCTCTCTATGACTGGCCGCTGACT 389
QY      101 AlaGluValProProGlnLeuLeuAlaAlaIaGlyPhePheHisThrGlyHisGlnAsp 120
Db      390 GCTGAGTGCCACCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      450 AAGGTGAGTGCTCTCTCTCTGCTATGGGGGCTGACAGACTGGAAGCGGGGAGACACCC 509
QY      141 TrpThrGlnHisAlaIysTrpPheProSerCysGlnPheLeuLeuAlaArgSerLysGly 160
Db      510 TGGACGGAGCATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 569
QY      161 AspPheValHisSerValGlnGlnIleThrHisSerGlnLeuGlnGlySerTrpAspProTrp 180
Db      570 GACTTTGTCCACAGTGTCCAGAGACTCACTCCAGCTGCTGGGCTCTGGGACCCGCTGG 629
QY      181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db      630 GAAGAACCGGAAGACGACAGCCCTGTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 689
QY      201 LeuProThrPro 204
Db      690 CTGCCACACCC 701
```

```

RESULT 7
BUI50825          918 bp      mRNA      linear      EST 03-SEP-2002
LOCUS             AGENCOURT_8712345 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6295194
DEFINITION        5', mRNA sequence.
ACCESSION         BUI50825
VERSION           BUI50825.1 GI:22664357
KEYWORDS
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2501 row: a column: 19
High quality sequence stop: 582.
Location/Qualifiers
1..918
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6295194"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1 05e-173 Length: 918
Score: 192.00 Matches: 192
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 62.1% Indels: 0
Gaps: 0
US-09-762-577b-12 (1-309) x BUI50825 (1-918)
QY 25 ProThGlnGluAryGyGlyProArySerLeuGlySerProValLeuGlyLeuAAspThr 44
Db 2 CCACCCAGAGAGGAGCTGTGACCCCGCTCTGTGGCAGCCCTGTCTAGGCTTGACACC 61
QY 45 CysATGAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuAryProLeuThrGlu 64
Db 62 TGCAGAGCTGTGAGACCACTGTGATGGCAGATCCCTGGCCAGCTGGCCGCCCTTGACAGAG 121
QY 65 GluGluGluGluGluGlyValAGlValAThrLeuSerAryGlyProAlaAAspProGlyMet 84
Db 122 GAGGAAGAGAGAGAGAGGCGCGCGGCACCTTGTCCAGGGAGGCTGCTCCCGGAGATG 181
QY 85 GlySerGluGluLeuAryGluAAspSerPheTyrAspTTPProLeuThrAlaGluValPro 104
Db 182 GGCTCTGAGAGATGCTGCTGCGCTCTTATGACTGGCGCTGACTGCTGAGGTGCCA 241

```

```

QY 105 ProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAAspIysValAryCys 124
Db 242 CCCGAGCTGCTGCTGCTGCTGCGGCTTCTTCCACACAGGCCATCAGACCAAGTGAAGTGC 301
QY 125 PhePheCysTyrGlyGlyLeuGlnSerTrpIysAryGlyAAspAAspProTyrThrGluHis 144
Db 302 TTCTCTGCTATGGGGGCGCTGCAGAGCTGGAAGGCGGGAGCGACCCCTGACGAGACAT 361
QY 145 AlalySTPPheProSerCysGlnPheLeuLeuArySerIysGlyAryAAspPheValHis 164
Db 362 GCAAGTGTTCCTCCAGCTGTACGTTCTGCTCCGTCMAAAGAGAGACTTGTGTCCAC 421
QY 165 SerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTyrPgluGluProGlu 184
Db 422 AGTGTGAGAGAGACTCACTCCACACTGCTGGGCTCTCTGGACCCCTGGAGAAACCGGAA 481
QY 185 AspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGluLeuProThrPro 204
Db 482 GACGAGGCGCTGTGGCCCTCCCTCCGTCCTGCTGAGTACCCTGAGCTGCCACGCC 541
QY 205 ArgAryGluValGlnSerGlySerAlaGlnGluPro 216
Db 542 AGGAGAGAGTCCAGTCTGAAGTCCCAAGAGCCA 577
RESULT 8
BGI68992          740 bp      mRNA      linear      EST 15-MAY-2001
LOCUS             602742920F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4872605 5',
DEFINITION        mRNA sequence.
ACCESSION         BGI68992
VERSION           BGI68992.1 GI:14079645
KEYWORDS
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 740)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1749 row: g column: 06
High quality sequence stop: 740.
Location/Qualifiers
1..740
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4872605"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
ORIGIN

```


Alignment Scores:

Pred. No.:	5 53e-169	Length:	740
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	60.5%	Indels:	0
DB:	2	Gaps:	0

US-09-762-577B-12 (1-309) x BG768992 (1-740)

```
OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 44 ATGGGACCTTAAAGACAGTGCACAGTGCCTGCACCTTGACCAACAGCCAGCCTGGGCA 103
OY 21 AlaGlyAspGlyProThrGlnGlnLysGlyProArgSerLeuGlySerProValLeu 40
Db 104 GCCGGTGAATGCTCCACCCAGAGAGCGCTGTGACCCCTCTCTGGGAGCCCTTCTCTA 163
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 164 GGCTTGGACACCTGCAGAGCCTGGGACCACTGGATGGCAATCTGGGAGCTGGCG 223
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 224 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 283
OY 81 PheProGlyMetGlySerGlyGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
Db 284 TTCCCGGCGCATGGGCTCTGAGAGATGGCTGCTGCTGCTCTCTCTCTCTCTCTCTCT 343
OY 101 AlaGlnValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 344 GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 403
OY 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnGlnGlnGlnGlnGlnGlnGln 140
Db 404 AAGGTGAGAGTGTCTTCTGCTATGGGGCCCTGCAGACCTGGAAGCGGGGAGCAGACCC 463
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 464 TGGACGAGCATGCGCAAGTGGTCCCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
OY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 524 GACTTTGTCCACAGTGTCCAGAGACTCCTCCAGCTGCTGCTGCTGCTGCTGCTGCTG 583
OY 181 GlnGluProGlnAspAlaAla 187
Db 584 GAAGAACCGGAAGACGCGCC 604
```

RESULT 9
BG770075 877 bp mRNA linear EST 15-MAY-2001
LOCUS 602745008F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4878193 5',
DEFINITION mRNA sequence.
ACCESSION BG770075
VERSION BG770075.1 GI:14080728
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 877)
REFERENCE 1 NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:

http://image.lnl.gov

Plate: L1CML1763 row: p column: 02

High quality sequence stop: 819.

FEATURES

source

```
1..877
/mol_type="mRNA"
/db_xref="taxon:9606"
/c1one="IMAGE:4878193"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/c1one_id="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; site 1: XhoI; site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

```

ORIGIN

Alignment Scores:

Pred. No.:	6.49e-169	Length:	877
Score:	187.00	Matches:	187
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	60.5%	Indels:	0
DB:	2	Gaps:	0

US-09-762-577B-12 (1-309) x BG770075 (1-877)

```
OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 55 ATGGGACCTTAAAGACAGTGCACAGTGCCTGCACCTTGACCAACAGCCAGCCTGGGCA 114
OY 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
Db 115 GCCGGTGAATGCTCCACCCAGAGAGCGCTGTGAGACCCGCTCTCTGGGAGCCCTGTCT 174
OY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 175 GGCTTGGACACCTGCAGAGCCTGGGACCACTGGATGGCAGATCTGGGGCAGCTGCGG 234
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 235 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294
OY 81 PheProGlyMetGlySerGlyGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
Db 295 TTCCCGGCGCATGGGCTCTGAGAGTTCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 354
OY 101 AlaGlnValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 355 GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 414
OY 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnGlnGlnGlnGlnGlnGlnGln 140
Db 415 AAGGTGAGAGTGTCTTCTGCTATGGGGCCCTGCAGAGCTGGAAGCCGGGAGCGAGCCC 474
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 475 TGGACGAGCATGCGCAAGTGTCCAGAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTG 534
OY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 535 GACTTTGTCCACAGTGTCCAGAGACTCCTCCAGCTGCTGCTGCTGCTGCTGCTGCTG 594
OY 181 GlnGluProGlnAspAlaAla 187
```

Db 595 GAAGACCGAGACGACGCC 615

RESULT 10
BUI68025

LOCUS BUI68025 956 bp mRNA linear EST 04-SEP-2002

DEFINITION AGENCOURT_8044840 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6088898 5', mRNA sequence.

ACCESSION BUI68025

VERSION BUI68025.1 GI:22682009

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsaps-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LNCM2327 row: n column: 03
High quality sequence start: 22
High quality sequence stop: 574.
Location/Qualifiers

FEATURES
Source

1. .956
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6088898"
/issue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 5.9e-167 Length: 956
Score: 185.00 Matches: 185
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.9% Indels: 0
DB: 5 Gaps: 0

US-09-762-577B-12 (1-309) x BUI68025 (1-956)

QY 24 GYPTGThGInGInuAGCyGgIProARSerLeuGlySerProValLeuGlyLeuAsp 43
DB 32 GGTCACACGAGAGGCTGTGAGACCCGCTCTCTGGGACAGCCCTCTTGGGCTTGAC 91
QY 44 ThrCyARAlATrAspHisValAspGlyGlnIleLeuGlyGlnLeuArgProLeuThr 63
DB 92 ACTCTGAGAGCTGTGGACCACTGTGATGGGCGATCTGGGCGACCTCGGCGCCCTGACA 151
QY 64 GInGInGInGInGInGInGInGInGInGInGInGInGInGInGInGInGInGInGIn 83
DB 152 GAGGAGAAAG 211
QY 84 MetGlySerGInGInGInGInGInGInGInGInGInGInGInGInGInGInGInGIn 103

Db 212 ATGGGCTGTGAGAGATTGCTGCTGCTCTTCTTATGCTGACCGCTGACTGTAGGTG 271
QY 104 ProProGInLeuLeuAl 123
DB 272 CCACCGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 331
QY 124 CysPhePheCysTyTyGlyGlyLeuGlnSerTrpIysAspGlyIAspAspProTrpThrGlu 143
DB 332 TGCTTCTTCTGTATAGGGGGCTGTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAG 391
QY 144 HisAlAlAlTrpPheProSerCysGlnPheLeuLeuArgSerIysGlyIAspAspPheVal 163
DB 392 CATGCCAAGTGTTCCTCCAGCTGTCAAGTTCCTGCTCCGGTCAAAAGAGAGACTTTGTC 451
QY 164 HisSerValGInGInuThHisSerGInLeuLeuGlnGlySerTrpAspProTrpGluPro 183
DB 452 CACAGTGTGACGAGAGACTCACTCCAGCTGCTGGGCTTCCTGGGACCCGTGGAAAGAACCG 511
QY 184 GInAspAl 203
DB 512 GAAGACGAGCCCTGTGGGCCCCCTCCGCTCCCTCCCTGCTGCTGCTGCTGCTGCTG 571
QY 204 ProArgArgGInuVal 208
DB 572 CCCAGAGAGAGGTC 586

RESULT 11
BUI72109 956 bp mRNA linear EST 04-SEP-2002
LOCUS BUI72109
DEFINITION AGENCOURT_7954295 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:610915 5', mRNA sequence.

ACCESSION BUI72109

VERSION BUI72109.1 GI:22686093

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsaps-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LNCM2356 row: 1 column: 20
High quality sequence stop: 535.
Location/Qualifiers

FEATURES
Source

1. .956
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:610915"
/issue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4,15e-163 Length: 956
 Score: 181.00 Matches: 181
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 58.6% Indels: 0
 Gaps: 0

US-09-762-577b-12 (1-309) x BUI1872109 (1-956)

```

OY 1 MetGIyProLyAspSerAlaLyScyLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 64 ATGGACCTTAAGAGAGCTGCCAAGTGCCTGCAACCTGACACACCCAGCCACTGGGCA 123
OY 21 AlaGIyAspGIyProThrGlnGlnuArgCySGIyProArgSerLeuGIySerProValIleu 40
DB 124 GCGCGTGAATGTCACACGAGAGCGCTGTGGACCCGCTCTCTGGCAGCCCTGCTTA 183
OY 41 GYLeuAspThrCyAArgAlaTrpAspHisValAspGIyGlnIleuGIyGlnLeuArg 60
DB 184 GGCCTGAGACCTGAGAGAGCTGGAGACCACTGATGGGAGATCTGGGCGACGTCGGG 243
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 244 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
OY 81 PheProGIyMetGIySerGIyGlnGlnLeuArgLeuAlaSerPheTyAspTrpProLeuThr 100
DB 304 TTCCCGGCGATGGGCTGTGAGAGATGGTGGCTCTGCTCTCTATAGATGGGCGCTGACT 363
OY 101 AlaGIyValProProGIyLeuLeuLeuAlaAlaGIyPhePheHisThrGIyHisGlnAsp 120
DB 364 GCTGAGGGGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
OY 121 LysValArgCySPhePheCySerGIyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
DB 424 AAGGTGAGGTGCTTCTTCTGCTATGGGGGCTGCGAGAGCTGAGAGCGGGGAGACACCC 483
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCySGlnPheLeuLeuArgSerIySGIyArg 160
DB 484 TGGAGGAGAGCATGCGAAGTGGTTCCCGAGCTGTCACTTCTGCTCGGCTCAAAAGAGAA 543
OY 161 AspPheValHisSerValGlnGlnuThrHisSerGlnLeuLeuGIySerTrpAspProTrp 180
DB 544 GACTTTGTCCACAGTGTGAGAGAGACTCACTCCAGCTGGGGCTCTGGGAGACCCGTGG 603
OY 181 Gln 181
DB 604 GAA 606

```

RESULT 12

BUI18703 958 bp mRNA linear EST 04-SEP-2002
 LOCUS BUI18703 7962186 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6106302
 DEFINITION AGENCOURT 7962186 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6106302
 5' mRNA sequence.

ACCESSION BUI18703
 VERSION BUI18703.1 GI:22702687
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eumetaria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 958)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LUNL at:
 http://image.llnl.gov
 Plate: L1CM2347 row: c column: 07
 High quality sequence start: 12
 High quality sequence stop: 611.
 Location/Qualifiers
 1..958
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6106302"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_112"
 /note="Organ: skin; Vector: pOTB7, Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4,15e-163 Length: 958
 Score: 181.00 Matches: 181
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 58.6% Indels: 0
 Gaps: 0

US-09-762-577b-12 (1-309) x BUI18703 (1-958)

```

OY 1 MetGIyProLyAspSerAlaLyScyLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 205 ATGGACCTTAAGAGAGCTGCCAAGTGCCTGCAACCTGACACACCCAGCCACTGGGCA 264
OY 21 AlaGIyAspGIyProThrGlnGlnuArgCySGIyProArgSerLeuGIySerProValIleu 40
DB 265 GCGCGTGAATGTCACACGAGAGCGCTGTGGACCCGCTCTCTGGCAGCCCTGCTTA 324
OY 41 GYLeuAspThrCyAArgAlaTrpAspHisValAspGIyGlnIleuGIyGlnLeuArg 60
DB 325 GGCCTGAGACCTGACAGAGCTGGAGACCACTGATGGGAGATCTGGGCGACCTGGG 384
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 385 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444
OY 81 PheProGIyMetGIySerGIyGlnGlnLeuArgLeuAlaSerPheTyAspTrpProLeuThr 100
DB 445 TTCCCGGCGATGGGCTGTGAGAGATGGTGGCTCTGCTCTCTATAGATGGGCGCTGACT 504
OY 101 AlaGIyValProProGIyLeuLeuLeuAlaAlaGIyPhePheHisThrGIyHisGlnAsp 120
DB 505 GCTGAGGTGCCACCCGAGCTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 564
OY 121 LysValArgCySPhePheCySerGIyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
DB 565 AAGGTGAGGTGCTTCTTCTGCTATGGGGGCTGCGAGAGCTGGAAGCGGGGAGAGACCC 624
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCySGlnPheLeuLeuArgSerIySGIyArg 160
DB 625 TGGAGGAGAGATGCGAAGTGGTTCCCGAGCTGTCACTTCTGCTCGGCTCAAAAGAGAA 684
OY 161 AspPheValHisSerValGlnGlnuThrHisSerGlnLeuLeuGIySerTrpAspProTrp 180
DB 685 GACTTTGTCCACAGTGTGAGAGAGACTCACTCCAGCTGGGGCTCTGGGAGACCCGTGG 744
OY 181 Gln 181

```

Db 745 GAA 747

RESULT 13
BM696272

LOCUS 603 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-DWO-agl-c-11-0-UI-r1 UI-E-DWO Homo sapiens cDNA clone

ACCESSION BM696272
VERSION BM696272.1 GI:19009530

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE 1 (bases 1 to 603)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL PUBMED
8889548

COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES
Source
Location/Qualifiers
1..603
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-DWO-agl-c-11-0-UI"
/tissue_type="lens"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DWO"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-DWO is a cDNA library containing the following
tissue(s): lens. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCAATGCGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."

ALIGNMENT SCORES:
Pred. No.: 2.45e-162 Length: 603
Score: 180.00 Matches: 180
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 58.3% Indels: 0
Gaps: 0
DB: 3

US-09-762-577b-12 (1-309) x BM696272 (1-603)

Qy 1 MetGlyProlyAspSerAlaIysCysIeuHIsarGlyProGlnProSerHisTrrAla 20
Db 43 ATGGAGCTTAAAGACAGATGCCAATGCTCTGCACCTGGACCAAGCCAGCCATCGGCA 102

Qy 21 AAGIYAspGlyProThrGlnGluArgCysGlyProAgsSerIeuGlySerProValIeu 40
Db 103 GCCGGTGAATGATGCCACCGAGAGAGCGCTGTGAGCCCGCTCTGGGCAAGCCCTGTCTTA 162

Qy 41 GILYLeuAspThrCysArgAlaITrrAspHisValAspGlyGlnIleuGlyGlnLeuArg 60
Db 163 GGCCTGGACACCTGCAGAGCTGGGACCACTGATGGGCAGATCTCGGCGCACTCGG 222

Qy 61 ProLeuThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db 223 CCCCTGACAG 282

Qy 81 PheProGlyMetGlySerGluGluIleuArgIleuAspPheTyrAspTrrProLeuThr 100
Db 283 TTCCCCGGCATGGGCTCTGAGAGAGTTCGTCGCTCTTCTATGACTGGCCGCTGACT 342

Qy 101 AAGIValProProGluLeuLeuAlaAlaAlaGlyPhePheHisTrrGlyHisGlnAsp 120
Db 343 GCTGAGGTGCCACCCGAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 402

Qy 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrrPysArgGlyAspAspPro 140
Db 403 AAGGTAGGTGCTCTTCTGCTATGGGGGCTGCAGAGCTGGAAGCCGGAGGACGACCCC 462

Qy 141 TrrPthrGlnHisAlaIysTrrPheProSerCysGlnPheLeuLeuArgSerIysGlyArg 160
Db 463 TGGACGGACATGGCAAGATGATGCTCCGAGCTGCAGTTCCTGCTCCGGTCAAAAGAGAA 522

Qy 161 AspPheValHisSerValGlnGluThrHisSerGlnIleuLeuGlySerTrrAspProTrr 180
Db 523 GACTTGTCCACAGTGTGCAGAGAGATCACTCCCACTGCTGGGCTCTGGAGCCCGTGG 582

RESULT 14
LOCUS B0877438 870 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8042576 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6090222
5', mRNA sequence.
ACCESSION B0877438
VERSION B0877438.1 GI:22269446
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE 1 (bases 1 to 870)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgabbs-r@mail.nih.gov
JOURNAL Tissue Procurement: DCTD/DRP
COMMENT Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LCM231 row: e column: 07
High quality sequence stop: 580.

FEATURES
Source
Location/Qualifiers
1..870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6090222"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2,446-158	Length:	870
Score:	176.00	Matches:	176
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	57.0%	Indels:	0
DB:	5	Gaps:	0

US-09-762-577B-12 (1-309) x B06877438 (1-870)

```
QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAla 20
Db 64 ATGGACCTTAAAGACAGTGCACAGTGCCTGCACCGTGACACACAGCCAGCCACTGGGACA 123
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 124 GCGGATATGATGCTCCACGACGAGGAGGCTGTGAGACCCCTCTCTGGGAGAGCCCTGTCTTA 183
QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 184 GGCTTGACACCTGCAGAGGCTGGAGCCACCTGATGGAGATCTTGGCCAGCTGGCG 243
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 244 CCCCCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThr 100
Db 304 TTCCCGGATGGGCTGTGAGAGAGTGGCTGTGCTCTCTCTCTGATGACTGGCCCTGACT 363
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 364 GCTAGAGTGCACCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTTPLeuArgGlyAspAspPro 140
Db 424 AAGCTGAGTGTCTTCTCTCTATGGGGGCTGACAGACTGGAAGCGGGGAGAGAGAGAGAG 483
QY 141 TrpThrGlnHisAlaLysTTPPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
Db 484 TGGACGAGAGTGCACAGTGGTGTCCCGACAGTGTCAATCCCGGTCAAAAGAGAGA 543
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 176
Db 544 GACTTTGTCACAGTGTGCAGAGACTCACTCCAGCTGCTGGGCTCC 591
```

RESULT 15

B0682378

LOCUS

AGENCOURT 8185884 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6263255

5' mRNA sequence.

B0682378

B0682378.1 GI:21795057

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 912)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabos-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LNCM2426 row: n column: 24
High quality sequence stop: 609.

FEATURES

source

1. 912

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6263255"

/tissue_type="melanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2,556-158	Length:	912
Score:	176.00	Matches:	176
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	57.0%	Indels:	0
DB:	5	Gaps:	0

US-09-762-577B-12 (1-309) x B0682378 (1-912)

```
QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTTPAla 20
Db 64 ATGGACCTTAAAGACAGTGCACAGTGCCTGCACCGTGACACACAGCCAGCCACTGGGACA 123
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 124 GCGGATATGATGCTCCACGACGAGGAGGCTGTGAGACCCCTCTCTGGGAGAGCCCTGTCTTA 183
QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 184 GGCTTGACACCTGCAGAGGCTGGAGCCACCTGATGGAGATCTTGGGCTCAGCTGGCG 243
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 244 CCCCCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
QY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThr 100
Db 304 TTCCCGGATGGGCTGTGAGAGAGTGGCTGTGCTCTCTCTCTGATGACTGGCCCTGACT 363
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 364 GCTAGAGTGCACCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTTPLeuArgGlyAspAspPro 140
Db 424 AAGCTGAGTGTCTTCTCTCTATGGGGGCTGACAGACTGGAAGCGGGGAGAGAGAGAGAG 483
QY 141 TrpThrGlnHisAlaLysTTPPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
Db 484 TGGACGAGAGTGCACAGTGGTGTCCCGACAGTGTCAATCCCGGTCAAAAGAGAGA 543
QY 161 AspPheValHisSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 176
```

Db 544 GACTTTGTCCACAGTGTGCAGAGACTCACTCCCACTGCTGCTCC 591

Search completed: April 24, 2006, 11:15:00
JOB time : 4516 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2006, 09:59:47 ; Search time 161 Seconds
(without alignments)
3411.593 Million cell updates/sec

Title: US-09-762-577B-12
Perfect score: 309
Sequence: 1 MGPRDSAKCHRGPPSHWA.....GLSGGLPAPLCLFWTVMAC 309

Scoring table: QUITGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size: 3
Total number of hits satisfying chosen parameters: 2599969

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Command line parameters:

-MODL=frame+ p2n model -DEV=xlh
-Q=/abs/ABSSWB pool/US09762577/runat 24042006 105928 1006/app query.fasta.1
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2nol1.rnt -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdt
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs06h
-USER=US09762577 @CGN 1 1 143 @runat 24042006 105928 1006 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Issued Patents NA:*

1: /cgnt2_6/ptodata/1/ina/1.COMB.seq:*
2: /cgnt2_6/ptodata/1/ina/5.COMB.seq:*
3: /cgnt2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgnt2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgnt2_6/ptodata/1/ina/H.COMB.seq:*
6: /cgnt2_6/ptodata/1/ina/PC/US.COMB.seq:*
7: /cgnt2_6/ptodata/1/ina/PP.COMB.seq:*
8: /cgnt2_6/ptodata/1/ina/RE.COMB.seq:*
9: /cgnt2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280	90.6	1260	3	US-09-949-016-1949
2	217	70.2	1337	3	US-09-127-928-1
3	117	37.9	8572	3	US-09-949-016-13691
4	68	22.0	601	3	US-09-949-016-66130
5	58	18.8	601	3	US-09-949-016-66140
6	49	15.9	601	3	US-09-949-016-66139
7	44	14.2	226	3	US-09-023-655-334
8	33	10.7	601	3	US-09-949-016-66134
9	30	9.7	200	3	US-09-016-434-216

10	30	9.7	200	3	US-09-023-655-387	Sequence 387, App
11	29	9.4	601	3	US-09-949-016-66138	Sequence 66138, A
12	28	9.1	601	3	US-09-949-016-66135	Sequence 66135, A
13	28	9.1	601	3	US-09-949-016-66136	Sequence 66136, A
14	27	8.7	601	3	US-09-949-016-66131	Sequence 66131, A
15	26	8.4	601	3	US-09-949-016-66137	Sequence 66137, A
16	26	8.4	601	3	US-09-949-016-21029	Sequence 21029, A
17	14	4.5	601	3	US-09-949-016-176073	Sequence 176073, A
18	14	4.5	1435	6	PCT-US95-05922A-1	Sequence 1, Appl1
19	14	4.5	1601	3	US-09-023-655-497	Sequence 497, App
20	14	4.5	2416	3	US-09-201-936-41	Sequence 41, Appl
21	14	4.5	2416	3	US-09-011-356-41	Sequence 41, Appl
22	14	4.5	2416	3	US-09-672-717-228	Sequence 228, App
23	14	4.5	2416	3	US-09-201-932-41	Sequence 41, Appl
24	14	4.5	2563	3	US-09-016-434-1076	Sequence 1076, App
25	14	4.5	2563	3	US-09-023-655-894	Sequence 894, App
26	14	4.5	2580	2	US-08-511-485-7	Sequence 7, Appl1
27	14	4.5	2580	3	US-09-201-936-7	Sequence 7, Appl1
28	14	4.5	2580	3	US-09-011-356-7	Sequence 7, Appl1
29	14	4.5	2580	3	US-09-672-717-222	Sequence 222, App
30	14	4.5	2580	3	US-09-201-932-7	Sequence 7, Appl1
31	14	4.5	2589	3	US-08-569-749-1	Sequence 1, Appl1
32	14	4.5	2589	3	US-09-689-366-1	Sequence 1, Appl1
33	14	4.5	2589	3	US-10-232-286-1	Sequence 1, Appl1
34	14	4.5	2589	6	PCT-US96-12860-1	Sequence 1, Appl1
35	14	4.5	2601	3	US-08-569-749-3	Sequence 3, Appl1
36	14	4.5	2601	3	US-09-689-366-3	Sequence 3, Appl1
37	14	4.5	2601	3	US-10-232-286-3	Sequence 3, Appl1
38	14	4.5	2601	6	PCT-US96-12860-3	Sequence 3, Appl1
39	14	4.5	2862	3	US-08-569-749-13	Sequence 13, Appl
40	14	4.5	2862	3	US-09-689-366-13	Sequence 13, Appl
41	14	4.5	2862	3	US-10-232-286-13	Sequence 13, Appl
42	14	4.5	2862	6	PCT-US96-12860-13	Sequence 13, Appl
43	14	4.5	3076	2	US-09-205-144-1	Sequence 1, Appl1
44	14	4.5	3076	3	US-09-814-915A-11	Sequence 11, Appl
45	14	4.5	3151	3	US-09-212-971-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-1949
Sequence 1949, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1949

LENGTH: 1260
TYPE: DNA
ORGANISM: Human

US-09-949-016-1949

Alignment Scores:

Pred. No.: 1,996-259
Score: 280.00
Percent Similarity: 100.0%
Best Local Similarity: 100.6%
Query Match: 90.6%
DB: 3
Length: 1260
Matches: 1260
Conservative: 280
Mismatch: 0
Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-1949 (1-1260)

```

QY      1 MetGlyProLysAspSerAlaLysCysLeuHisArgIlyProGlnProSerHisTrpAla 20
Db      174 ATGGGACCTTAAGACAGTGTCCAAAGTGTCCGACCGTGGACCAACAGCCAGCAGCCTGGACA 233
QY      21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProAspSerLeuGlySerProValLeu 40
Db      234 GCCGGTGAATGTCCTCCACGAGGAGCGCTGTGACCCCTCTCTGGGCGACCGCTGTCTTA 293
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      294 GGCCCTGACACCTCGACAGAGCTGGAGCACCGTGAATGGCGAGATCCCTGGCGACCTCGG 353
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81 PheProGlyMetGlySerGlyGlnGlnArgLeuAlaSerPheTrpAspTrpProLeuThr 100
Db      414 TTCCCGGCGATGGGCTCTGAGAGAGTGTGCTGTGCTCTCTCTATGAGTGGCGCTGACT 473
QY      101 AlaGlyValAlaProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      474 GCTGAGTGGCCACCCGAGCTGTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 533
QY      121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      534 AAGGTGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 593
QY      141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      594 TGGACGAGAGCTGTCCAGTGTGTCTCCAGCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCT 653
QY      161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      654 GACTTGTCCACAGTGTGTCCAGAGACTCTCCAGCTGTGTGCTGTGTGCTGTGTGCTGTGTG 713
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db      714 GAAGAACCGGAAGACGACGCCCTGTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 773
QY      201 LeuProThrProArgAlaGlyValAlaGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
Db      774 CTGCCCCACACCCAGAGAGAGTCCAGTCTGAAGAGTCCAGAGAGCCAGAGAGCCAGAGAT 833
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      834 GTGAGGCGCAGCTGCGCGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY      241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db      894 GCCGTGTCACTGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
QY      261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      954 CTGCAGCTGTGCCCCATCTGCAAGGCCCGCTCCGACCGCGGTGCGACCTCTCTGTGCC 1013

```

RESULT 2
US-09-127-928-1

```

; Sequence 1, Application US/09127928
; Patent No. 6472172
; GENERAL INFORMATION:
; APPLICANT: Deng, Gang
; APPLICANT: Lin, Jiling-Huey
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Protein
; TITLE OF INVENTION: DNA Encoding a No. 6472172el Human Inhibitor-of-Apoptosis
; FILE REFERENCE: DNA Encoding HIAP3
; CURRENT APPLICATION NUMBER: US/09/127,928
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 1
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)..(1066)
US-09-127-928-1

```

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
1	217.00	1337	217
Best Local Similarity:	100.0%	Conservative:	0
Query Match:	100.0%	Mismatches:	0
DB:	70.2%	Indels:	0
	3	Gaps:	0

US-09-762-577B-12 (1-309) x US-09-127-928-1 (1-1337)

```

QY      1 MetGlyProLysAspSerAlaLysCysLeuHisArgIlyProGlnProSerHisTrpAla 20
Db      170 ATGGGACCTTAAGACAGTGTCCAAAGTGTCCGACCGTGGACCAACAGCCAGCAGCCTGGACA 229
QY      21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProAspSerLeuGlySerProValLeu 40
Db      230 GCCGGTGAATGTCCTCCACGAGGAGCGCTGTGACCCCGCTCTGTGGGCGACCGCTGTCTTA 289
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      290 GGCCCTGACACCTCGACAGAGCTGGAGACAGTGAATGGAGAGATCTGTGGCGCCAGCTGGCG 349
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      350 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 409
QY      81 PheProGlyMetGlySerGlyGlnGlnArgLeuAlaSerPheTrpAspTrpProLeuThr 100
Db      410 TTCCCGGCGATGGGCTCTGAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 469
QY      101 AlaGlyValAlaProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      470 GCTGAGTGGCCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 529
QY      121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      530 AAGGTGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 589
QY      141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db      590 TGGACGAGAGATGCCAAAGTGTTCCTCCAGCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCT 649
QY      161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      650 GACTTGTCACTGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db      710 GAAGAACCGGAAGAGCAGACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
QY      201 LeuProThrProArgAlaGlyValAlaGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 217
Db      770 CTGCCCCACACCCAGAGAGAGTCCAGTCTGAAGTGTCCAGAGAGCCAGAGAGCCAGAG 820

```

RESULT 3

```

US-09-949-016-13691
; Sequence 13691, Application US/09949016
; Patent No. 6812359
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016

```



```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13691
; LENGTH: 8572
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13691

Alignment Scores:
Pred. No.: 4,58e-102 Length: 8572
Score: 117.00 Matches: 117
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 37.9% Indels: 0
DB: 3 Gaps: 0

US-09-762-577b-12 (1-309) x US-09-949-016-13691 (1-8572)

Qy 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 2174 ATGGGACCTTAAAGACAGTGCACAGTGCCTGCACCGTGCACACAGCCAGCCACTGGGCA 2233

Qy 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 2234 GCCGTGATGATGCTCCACCCAGAGAGCTGTGAGACCCCGCTCTCTGGGAGGCCCTGTCTTA 2293

Qy 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 2294 GGCCCTGACACCTGCAGAGAGCTGGGACACCGATGATGGGACATCTGGCCAGCTGGCG 2353

Qy 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 2354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2413

Qy 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyraAspTrpProLeuThr 100
Db 2414 TTCCCGGCGATGGGCTCTGAGAGAGTGGCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 2473

Qy 101 AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGly 117
Db 2474 GCTGAGGTGGCCACCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2524

RESULT 4
US-09-949-016-66130
; Sequence 66130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 66130
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66130
```

```

Alignment Scores:
Pred. No.: 4,26e-56 Length: 601
Score: 58.00 Matches: 58
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 18.8% Indels: 0
DB: 3 Gaps: 0

US-09-762-577b-12 (1-309) x US-09-949-016-66130 (1-601)

Qy 216 ProGlyAlaArgAspValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGln 235
Db 427 CCAGAGCCGAGGATGGAGGAGCGAGCTGCGCGGCTGCAGAGAGAGAGAGAGAGAGAGAG 486

Qy 236 ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeuValCysAla 255
Db 487 GTGTGCTGGACCGCGCGGTGCTCATCTGCTTTGTGCGCGGACCACTGCTGTGCT 546

Qy 256 GluCysAlaProGlyLeuGlnLeuCysProIleCysArgAlaProValArgSer 273
Db 547 GAGTGTGCTCCCGCGCTGCAGCTGTGCTCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAG 600

RESULT 5
US-09-949-016-66140
; Sequence 66140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 66140
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66140

Alignment Scores:
Pred. No.: 1,72e-46 Length: 601
Score: 58.00 Matches: 58
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 18.8% Indels: 0
DB: 3 Gaps: 0

US-09-762-577b-12 (1-309) x US-09-949-016-66140 (1-601)

Qy 110 AlaAlaGlyPhePheHisThrGly 117
Db 181 GCTGCGGCTTCTTCCACACAGGT 204
```

RESULT 6
US-09-949-016-66139
Sequence 66139, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66139
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-66139

Alignment Scores:
Pred. No.: 7.58e-38 Length: 601
Score: 49.00 Matches: 49
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 15.9% Indels: 0
DB: 3 Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66139 (1-601)

Qy 216 ProGlyAlaArgAspValGluAlaGlnLeuArgLeuGlnGluAlaArgThrCysLys 235
Db 455 CCAGAGCCGAGATGTGGAGGCGCAGCTCGCGGCTGCGAGAGAGAGAGCTGCAAG 514

Qy 236 ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeuValCysAla 255
Db 515 GTGGCTCGGACCGCGCGCTGTCCATGCTTTGTGCTGCGGCCACCTGGGTGTGCT 574

Qy 256 GluCysAlaProGlyLeuGlnLeuCys 264
Db 575 GAGTGTGCCCCCGCGCTGCGAGCTGTGC 601

RESULT 7
US-09-023-655-334
Sequence 334, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOT09
CLONE: 1419118
US-09-023-655-334

Alignment Scores:
Pred. No.: 1.9e-33 Length: 226
Score: 44.00 Matches: 44
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.2% Indels: 0
DB: 3 Gaps: 0

US-09-762-577B-12 (1-309) x US-09-023-655-334 (1-226)

Qy 97 TrpProLeuThrAlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThr 116
Db 95 TGCGCGCTGACTGCTGAGTGCCACCGAGCTGCTGCGGCTTCTTCCACACA 154

Qy 117 GlyHisGlnAspIleValArgCysPhePheCysTYrGlyGlyLeuGlnSerTrpIleArg 136
Db 155 GGCATCAGACAAAGTGAGTGCTTCTTCTGCTAAGGGGCTGACAGCTGGAAGCC 214

Qy 137 GlyAspAspPro 140
Db 215 GGGAGAGACCC 226

RESULT 8
US-09-949-016-66134
Sequence 66134, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66134
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-66134

Alignment Scores:
Pred. No.: 1.77e-22 Length: 601

Score:	33.00	Matches:	33
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	10.7%	Indels:	0
DB:	3	Gaps:	0

US-09-762-577B-12 (1-309) X US-09-949-016-66134 (1-601)

QY 117 GLYHSGINAspIysValArgCysPheCysTYRglYglYleuGlnSerTrpIysArg 136
 Db 332 GGCCATCAGACCAAGGTGAGGTGCTTCTTCGCTATGCGGGGCTGCAGAGCTGGAGAGGC 391

QY 137 GLYASPA SPProT rTpTh rGl uHi sAl aL yst rPhe Pro 149
 392 GGGGACGACCCCTGACGGAGCATGCCAAGTGGTCCCC 430
 Db

RESULT 9
US-09-016-434-216
; Sequence 216, Application US/09016434

```

; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
;

```

```

1  TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
2
3  NUMBER OF SEQUENCES:  1490
4
5  CORRESPONDENCE ADDRESS:
6
7  ADDRESS:  UNIVERSITY OF CALIFORNIA, TWO

```

STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

```

; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPILED: TUE DEC 10 1986 11:17

```

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;
; CURRENT APPLICATION DATA:
;
; ADDRESSATION NUMBER: MS/60/0035 424

```

```

;
; FILING DATE: HEREWITH
;
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER:

```

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (550) 357-0555

```

; TELEFAX: (650) 845-4166
;
; INFORMATION FOR SEQ ID NO: 216:
;
; SEQUENCE CHARACTERISTICS:
;
;     LENGTH: 200 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

```

LIBRARY: BLADTUT04
CLONE: 1520835
US-09-016-434-216

Alignment scores:	
Pred. No.:	4.74e-20
Score:	200
Percent Similarity:	30.00
Matches:	30
Conservative:	0

Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	9.7%	Indels:	0
DB:	3	Gaps:	0

US-09-762-577B-12 (1-309) x US-09-016-434-216 (1-200)

Oy 226 ArgArgLeuGlnGluGlnUrbThrCysLysValCysLeuAspArgAlaValSerIleVal 245
|||
Db 40 CGCGGCTGCAGSAGSAGACGTGCCAAGTGTCCTCGACCCGCCCTGTCTATCTC 99

OY 246 PheValProCysGlyHisIleuValCysAla 255
|||
Db 100 TTGTGCGCGGCACCTGGTCTGTGCT 129

RESULT 10
US-09-023-655-387
; Sequence 387, Application US/09023655

```

; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart

```

;	TITLE OF INVENTION:	COMPOSITION F
;	TITLE OF INVENTION:	EXPRESSION
;	NUMBER OF SEQUENCES:	1508

ADDRESSEE: INCYTE PHARMACEUTICAL
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO

```

;
;   COUNTRY:  USA
;   ZIP:  94304
;
;   COMPUTER READABLE FORM:
;
;   *****
;

```

```
;
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Word Perfect 6.1 for
;             OS/2 and Windows
```

; APPLICATION NUMBER: US/09/023,6
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIORITY INFORMATION:

; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ;

NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-000

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 387:

```

; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;

```

```

; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT04
; CLONE: 1520835
;

```

Alignment Scores:
Pred. No.: 4.74e-20
Score: 30.00

Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	9.7%

US-09-762-577B-12 (1-309) x US-09-023-6

Db 40 CGCGCGCTGCAGAGAGAGACGCTT

Db 100 TTGTGCGCTGCGGCGCAGCTGTGTGCT 129

RESULT 11

US-09-949-016-66138
Sequence 66138, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 66138

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-66138

Alignment Scores:

Pred. No.: 1,23e-18

Score: 29.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 9.4%

DB: 3

Gaps: 0

Length: 601

Matches: 29

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66138 (1-601)

QY 216 ProGlyAlaArgAppValGlnAlaGlnLeuArgArgLeuGlnGlnAlaArgThrCysLys 235

DB 515 CCAAGAGCCAGGATGTGGAGGCGGCGCTGCGGCTGCGAGAGAGAGAGCTGCAG 574

QY 236 ValCysLeuAspArgAlaValSerIle 244

DB 575 GTGTGCTGTGAGCGCGCGCTGTCTCATC 601

RESULT 12

US-09-949-016-66135

Sequence 66135, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 66135

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-66135

Alignment Scores:

Pred. No.: 1.13e-17

Score: 601

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 9.1%

DB: 3

Gaps: 0

Length: 601

Matches: 28

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66135 (1-601)

QY 150 SerCysGlnPheLeuLeuArgSerIysGlyArgAspPheValHisSerValGlnGluThr 169

DB 221 AGCTGTCACTTCTCTCTCGGTCAAAAGAGAGACTTTGTCCACAGTGTCCAGAGACT 280

QY 170 HisSerGlnLeuLeuGlySerIle 177

DB 281 CACTCCAGCTGTCTGCGCTTTGG 304

RESULT 14

US-09-949-016-66131

Sequence 66131, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 66131

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-66131

Alignment Scores:

Pred. No.: 1.13e-17

Score: 601

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 9.1%

DB: 3

Gaps: 0

Length: 601

Matches: 28

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66136 (1-601)

QY 150 SerCysGlnPheLeuLeuArgSerIysGlyArgAspPheValHisSerValGlnGluThr 169

DB 221 AGCTGTCACTTCTCTCTCGGTCAAAAGAGAGACTTTGTCCACAGTGTCCAGAGACT 280

QY 170 HisSerGlnLeuLeuGlySerIle 177

DB 281 CACTCCAGCTGTCTGCGCTTTGG 304

RESULT 14

US-09-949-016-66131

Sequence 66131, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 66131

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-66131

Alignment Scores:

Pred. No.: 1.13e-17

Score: 601

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 9.1%

DB: 3

Gaps: 0

Length: 601

Matches: 28

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-762-577B-12 (1-309) x US-09-949-016-66136 (1-601)

QY 150 SerCysGlnPheLeuLeuArgSerIysGlyArgAspPheValHisSerValGlnGluThr 169

DB 221 AGCTGTCACTTCTCTCTCGGTCAAAAGAGAGACTTTGTCCACAGTGTCCAGAGACT 280

QY 170 HisSerGlnLeuLeuGlySerIle 177

DB 281 CACTCCAGCTGTCTGCGCTTTGG 304

;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 66131
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-66131

Alignment Scores:

Pred. No.:	1,03e-16	Length:	601
Score:	27.00	Matches:	27
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	8.7%	Indels:	0
DB:	3	Gaps:	0

US-09-762-577B-12 (1-309) x US-09-949-016-66131 (1-601)

OY 91 LeuAlaSerPheTYrAspTrpProLeuThrAlaGluValProProGluLeuLeuAlaAla 110
Db 3 CTGGCTCTCTCTAAGACTGGCCGCTGACTGCTGAGTGCACCCGAGCTGCTGCTGCT 62

OY 111 AlaGlyPhePheHisThrGly 117
Db 63 GCCGGCTTCTTCCACACAGGT 83

RESULT 15

US-09-949-016-66137
; Sequence 66137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66137
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66137

Alignment Scores:

Pred. No.:	9.38e-16	Length:	601
Score:	26.00	Matches:	26
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	8.4%	Indels:	0
DB:	3	Gaps:	0

US-09-762-577B-12 (1-309) x US-09-949-016-66137 (1-601)

OY 193 ValProAlaSerGlyTYrProGluLeuProThrProArgArgGluValGlnSerGluSer 212
Db 349 GTCCCTGCTCTGGTACCTCGAGCTGCCACACCCAGAGAGAGTCAAGTCAAGT 408

OY 213 AlaGlnGluProGlyAla 218
Db 409 GCCCAGAGCCAGGTGCA 426

Search completed: April 24, 2006, 10:02:44
Job time : 166 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 24, 2006, 10:03:01; Search time 625 Seconds

(without alignments)
4088.380 Million cell updates/sec

Title: US-09-762-577b-12

Perfect score: 309
Sequence: 1 MGRPDSAKCHRGPSHWA.....GLOSGLPAPLCFTWTFMAC 309

Scoring table: 0.150

Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 60.0, Fgapext 7.0
Delop 60.0, Delext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word sizes: 1

Total number of hits satisfying chosen parameters: 19572550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=xlh
-O=/abs/ABSSWB.spool/US09762577/runat 24042006 105937 1201/app.query.fasta_1
-DB=Published Applications NA Main -OPMT=fastap -SUFFIX=p2nol1.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdt -LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs06h
-USER=US09762577 @CGN 1.1 797 @runat 24042006 105937 1201 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database: Published Applications NA Main:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280	90.6	843	5	US-10-244-586-2
2	280	90.6	1260	8	US-10-188-646-4
3	280	90.6	1268	8	US-10-807-897-28
4	280	90.6	1376	5	US-10-244-586-1
5	217	70.2	1168	6	US-10-188-646-12
6	217	70.2	1322	8	US-10-807-897-26
7	217	70.2	1337	5	US-10-235-026-1

8	217	70.2	1363	8	US-10-839-882-37	Sequence 37, Appl
9	177	57.3	1068	6	US-10-203-708-21	Sequence 21, Appl
10	149	48.2	449	8	US-10-723-660-4697	Sequence 4697, Ap
11	149	48.2	769	6	US-10-203-708-22	Sequence 22, Appl
12	131	42.4	858	8	US-10-723-660-8265	Sequence 8265, Ap
13	120	38.8	614	9	US-10-450-763-27354	Sequence 27354, A
14	120	38.8	615	7	US-10-296-115-63	Sequence 63, Appl
15	117	37.9	4810	6	US-10-188-646-11	Sequence 11, Appl
16	116	37.5	3782	9	US-10-450-763-27357	Sequence 27357, A
17	87	28.2	339	8	US-10-983-995-1	Sequence 1, Appl1
18	65	21.0	676	8	US-10-723-660-4448	Sequence 4448, Ap
19	54	17.5	404	9	US-10-779-543-12365	Sequence 12365, A
20	44	14.2	226	7	US-10-641-643-334	Sequence 1334, App
21	30	9.7	200	6	US-10-305-720-216	Sequence 216, App
22	30	9.7	200	7	US-10-641-643-387	Sequence 387, App
23	28	9.1	444	9	US-10-450-763-27355	Sequence 27355, A
24	26	8.4	720	5	US-10-027-632-14213	Sequence 14213, A
25	26	8.4	720	5	US-10-027-632-14214	Sequence 14214, A
26	26	8.4	720	6	US-10-027-632-14213	Sequence 14213, A
27	26	8.4	720	6	US-10-027-632-14214	Sequence 14214, A
28	26	8.4	721	5	US-10-027-632-145092	Sequence 145092, A
29	26	8.4	721	6	US-10-027-632-145092	Sequence 145092, A
30	15	4.9	698	5	US-10-027-632-145255	Sequence 145255, A
31	15	4.9	698	5	US-10-027-632-145255	Sequence 145255, A
32	15	4.9	698	5	US-10-027-632-145257	Sequence 145257, A
33	15	4.9	698	6	US-10-027-632-145255	Sequence 145255, A
34	15	4.9	698	6	US-10-027-632-145256	Sequence 145256, A
35	15	4.9	698	6	US-10-027-632-145257	Sequence 145257, A
36	14	4.5	372	7	US-10-242-535A-20989	Sequence 20989, A
37	14	4.5	372	7	US-10-085-783A-20989	Sequence 20989, A
38	14	4.5	460	3	US-09-960-352-8049	Sequence 8049, Ap
39	14	4.5	1400	2	US-10-956-157-5804	Sequence 5804, Ap
40	14	4.5	1435	5	US-08-464-588-1	Sequence 1, Appl1
41	14	4.5	1435	5	US-10-323-643-1	Sequence 1, Appl1
42	14	4.5	1601	7	US-10-641-643-497	Sequence 497, Appl
43	14	4.5	1857	9	US-10-975-974-41	Sequence 47, Appl
44	14	4.5	2416	3	US-09-201-936-41	Sequence 41, Appl
45	14	4.5	2416	7	US-10-636-065-228	Sequence 228, Appl

ALIGNMENTS

RESULT 1
US-10-244-586-2
; Sequence 2, Application US/10244586
; Publication No. US20030087319A1
; GENERAL INFORMATION:
; APPLICANT: COMES, BRUCE C.
; APPLICANT: KASOF, GARRETT M.
; APPLICANT: PROSSER, JUDITH C.
; TITLE OF INVENTION: NOVEL PROTEIN
; FILE REFERENCE: DJB/009901/0270799
; CURRENT APPLICATION NUMBER: US/10/244,586
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/594,119
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/139,291
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-586-2

Alignment Scores:
Pred. No.: 2,67e-273
Score: 280.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 90.6%
DB: 5
Length: 843
Matches: 280
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

```

US-09-762-577B-12 (1-309) x US-10-244-586-2 (1-843)
QY      1 MetGlyProLyAspSerAlaLeuHisArgGlyProGlnProSerHisTrpAla 20
Db      1 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGGACCAAGCCGAGCCACTGGGCA 60
QY      21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      61 GCCGGTATGATGCCACCGCAGAGCGCTGTGGACCCCGCTCTCGGGCAGCCCTGTCTTA 120
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      121 GGCTGGACACCTCAGAGCCTGGGACCACTGGATGGGAGATCCTGGGCCAGACTGGCG 180
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      181 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY      81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheThrAspTrpProLeuThr 100
Db      241 TTCCCGGCAATGGGCTGTAGAGAGTTGCTGTGGCTCTTCTATATGACTGGCCGTACT 300
QY      101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      301 GCTGAGGTGCACCCCGAGCTGCTGGCTGCCGCTTCTTCCACAGGCCATCAGAGAC 360
QY      121 LysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      361 AAGGTGAGGTGCTTCTTCTCTATAGGGGAGCTCTGAGAGCTGAGAGGCGAGGAGCAGC 420
QY      141 TrpThrGlnHisAlaAlaYsTrpPheProSerCysGlnPheLeuLeuArgSerIysGlyArg 160
Db      421 TGGACGAGGATGCGCAAGTGTTCCTCCAGCTGTCAATTCTGCTCCGGTCAAAAGGAA 480
QY      161 AspPheValHisSerValGlnGlnIleHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      481 GACTTTGTCCACAGTGTGCAGAGACTCACTCCACACTGCTGGCTCCCGGAGCCCGTGG 540
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db      541 GAAGAACCGGAGAACGACGAGCCCTGTGGCCCTCTGCTCCGCTGGATACCTTAG 600
QY      201 LeuProThrProArgArgGlnValAlaGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
Db      601 CTGCCCAACCCAGAGAGAGAGTCCAGTGTGAAGTCCAGAGCCAGAGCCAGGAGAT 660
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      661 GTGGAGCGCAGAGCTGGCGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY      241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlyCysAlaProGly 260
Db      721 GCGGTGTCCATGCTTTGTGTGGCGGCGCACCTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY      261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      781 CTGCAGCTGTGCCCATCTGCAGAGCCCGCGTCCGACCGCGTGGCAGCCTTCTGTGCC 840

RESULT 2
US-10-188-646-4
; Sequence 4, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF IL1V IN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 1260

```

```

; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174) ... (1016)
US-10-188-646-4

Alignment Scores:
Pred. No.: 3,75e-273 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conserved: 0
Best Local Similarity: 100.0% Mismatch: 0
Query Match: 90.6% Indels: 0
DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-188-646-4 (1-1260)
QY      1 MetGlyProLyAspSerAlaLeuHisArgGlyProGlnProSerHisTrpAla 20
Db      174 ATGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGGACCAAGCCGAGCCACTGGGCA 233
QY      21 AlaGlyAspGlyProThrGlnGlnArgCysGlyProArgSerLeuGlySerProValLeu 40
Db      234 GCCGGTATGATGCCACCGCAGAGCGCTGTGGACCCCGCTCTCGGGCAGCCCTGTCTTA 293
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db      294 GGCTGGACACCTCAGAGCCTGGGACCACTGGATGGGAGATCCTGGGCCAGCTGGCG 353
QY      61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db      354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY      81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheThrAspTrpProLeuThr 100
Db      414 TTCCCGGCAATGGGCTGTAGAGAGTTGCTGTGGCTCTTCTATATGACTGGCCGTACT 473
QY      101 AlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db      474 GCTGAGGTGCACCCCGAGCTGCTGGCTGCCGCTTCTTCCACAGGCCATCAGAGAC 533
QY      121 LysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db      534 AAGGTGAGGTGCTTCTTCTCTATAGGGGAGCTCTGAGAGCTGAGAGGCGAGGAGCAGC 593
QY      141 TrpThrGlnHisAlaAlaYsTrpPheProSerCysGlnPheLeuLeuArgSerIysGlyArg 160
Db      594 TGGACGAGGATGCGCAAGTGTTCCTCCAGCTGTCAATTCTGCTCCGGTCAAAAGGAA 653
QY      161 AspPheValHisSerValGlnGlnIleHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db      654 GACTTTGTCCACAGTGTGCAGAGACTCACTCCACAGCTGTGGCTCCCGGAGCCCGTGG 713
QY      181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGln 200
Db      714 GAAGAACCGGAGAACGACGAGCCCTGTGGCCCTCTGCTCCGCTGGATACCTTAG 773
QY      201 LeuProThrProArgArgGlnValAlaGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220
Db      774 CTGCCCAACCCAGAGAGAGTCCAGTGTGAAGTCCAGAGCCAGAGCCAGGAGAT 833
QY      221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      834 GTGGAGCGCAGAGCTGGCGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY      241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlyCysAlaProGly 260
Db      894 GCGGTGTCCATGCTTTGTGTGGCGGCGCACCTGTGTGTGTGTGTGTGTGTGTGTGT 953
QY      261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db      954 CTGCAGCTGTGCCCATCTGCAGAGCCCGCGTCCGACCGCGTGGCAGCCTTCTGTGCC 1013

```



```
RESULT 3
US-10-807-897-28
; Sequence 28, Application US/10807897
; Publication No. US20040192631A1
; GENERAL INFORMATION:
; APPLICANT: Xiang, Rong
; APPLICANT: Zhou, He
; APPLICANT: Reisfeld, Ralph A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-874.1
; CURRENT APPLICATION NUMBER: US/10/807,897
; PRIORITY FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,009
; PRIORITY FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1268
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1016)
US-10-807-897-28

Alignment Scores:
Pred. No.: 3.77e-273 Length: 1268
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x US-10-807-897-28 (1-1268)

OY 1 MetGlyProLyAspSerAlaLeuHisArgGlyProGlnProSerHisTTPAla 20
Db 174 ATGGGACCTAAAGACAGTGCACAGTGCCTGCACCGTGACACAGCCAGCCACTGGGCA 233
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCGCGTGAATGGTCCACCCAGAGGAGCGCTGTGACCCCGCTCTGTGGAGCCCTGTCTTA 293
OY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 294 GGCCTGGACACCTGACAGAGCGCTGGGACCACTGGATGGGAGATCTGGGCCAGCTGGCG 353
OY 61 ProLeuThrGlnGluGlnGluGlnGluGlnAlaGlyAlaThrLeuSerArgGlyProAla 80
Db 354 CCCCAGACAGAGGAGAGAGAGAGAGGCGCGCGGCGCCACCTGTCTCCAGGGGCGCTGCC 413
OY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThr 100
Db 414 TTCCCGGCAATGGGCTGTAGAGAGTGGTGGCTCTCTCTTATGACTGGCCCGTGACT 473
OY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGCCACCGGACCTGCTGCTGCCCTCTTCCACACAGGCCATCAAGAC 533
OY 121 LysValAlaGlyCysPhePheCysTyrGlyGlyLeuGlnSerTTPLeuArgGlyAspAspPro 140
Db 534 AAGGTGAGGTCTCTTCTGCTATGGGGCTGACAGACTGGAAGCCGGGGAGACAGACCC 593
OY 141 TrpThrGlnHisAlaValTTPPheProSerCysGlnPheLeuLeuArgSerLeuGlyValArg 160
Db 594 TGGACGGACATGCGCAAGTGTTCCTCCAGCTGTCTGCTCTCCGCTCAAAAGAGAA 653
OY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTTPAspProTTP 180
Db 654 GACTTGTTCACAGTGTCCAGAGAGACTCACTCCAGCTGCTGGGCTCTGGGACCCGTTGG 713
```

```
US-10-244-586-1
; Sequence 1, Application US/10244586
; Publication No. US20030087319A1
; GENERAL INFORMATION:
; APPLICANT: GOMES, BRUCE C.
; APPLICANT: KASOF, GARRETT M.
; APPLICANT: PROSSER, JUDITH C.
; TITLE OF INVENTION: NOVEL PROTEIN
; FILE REFERENCE: DB/009901/0270799
; CURRENT APPLICATION NUMBER: US/10/244,586
; PRIORITY FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/594,119
; PRIORITY FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/139,291
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-586-1

Alignment Scores:
Pred. No.: 4.04e-273 Length: 1376
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x US-10-244-586-1 (1-1376)

OY 1 MetGlyProLyAspSerAlaLeuHisArgGlyProGlnProSerHisTTPAla 20
Db 211 ATGGGACCTAAAGACAGTGCACAGTGCCTGCACCGTGACACAGCCAGCCACTGGGCA 270
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 271 GCCGCTGATGTCCACAGAGAGCGCTGTGAGACCCGCTCTCTGGGACGCCCTGTCTTA 330
OY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 331 GGCCTGACACCTGCAAGCCTGGAGACCACTGGATGGGACATCTCGGCGCAGCTGGCG 390
OY 61 ProLeuThrGlnGluGlnGluGlnGluGlnAlaGlyAlaThrLeuSerArgGlyProAla 80
Db 391 CCCCAGACAGAGGAGAGAGAGAGAGGCGCGGCGCCACCTTGTCTCAGGGGCGCTGCC 450
OY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTTPProLeuThr 100
```

Db	451	TTCCCGGCAATGGGCTCTGAGAGATTGGCTCTGGCCCTCTTATGACTGGCCGGTACT	510
QY	101	AlaGluValProProGluIuIeuIuAlaIaIaIaGlyPhePheHisThrGlyHisGlnAsp	120
Db	511	GCTAGAGTGCACCCGAGCTGCTGCTGCTGGCGGCTTCTTCCACACAGGCGCATAGAC	570
QY	121	LysValArgCysPhePheCysTyrGlyGlyIleuGlnSerTrpIlyValGlyValAspPro	140
Db	571	AAGGTAGAGTCTTCTTCTGCTGTAAGGGGGCCCTGCAGAACTGAAGCCGGGGAGACCC	630
QY	141	TyrThrGluHisAlaIuYsTrpPheProSerCysGlnPheIuIeuAlaGserLysGlyArg	160
Db	631	TGACGAGAGCATCCAAGTGTTCCCGACGTCTAGTTCTCTCCGGTCAAAAGGAAGA	690
QY	161	AspPheAlaHisSerValGlnGluThrHisSerGlnIuIeuGlnGlySerTyrAspProTrp	180
Db	691	GACTTGTCACAGTGTGAGAGAGACTCACTCCGACGTGCTGGGCTCTGGAGCCGTGG	750
QY	181	GluGluProGluAspAlaIaIaProValAlaProSerValProAlaSerGlyTyrProGlu	200
Db	751	GAGAACCGGAAACCCAGCCCTGTCGGCCCTCCGCTCGCTTGGGTACCTCGAG	810
QY	201	LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyValaAspArg	220
Db	811	CTGCCACACCCAGAGAGAGGTCCAGTCTAAAGTCCCAAGAGCCAGAGCCAGAGGAT	870
QY	221	ValGluAlaGlnLeuArgArgIleuGlnGlnGluArgThrCysLysValCysLeuAspArg	240
Db	871	GTAAGAGCCGAGCTGGCGGCTGCAGAGAGAGAGACGTGCAAGGTGTGCTCGACCCG	930
QY	241	AlaValSerIleValPheValProCysGlyHisIleuValCysAlaGluCysAlaProGly	260
Db	931	GCCGTTCATGTCCTTGTGTGCGCGGGCCACTGGTGTGTCGTAAGTGTGCCCCGGC	990
QY	261	IleuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer	280
Db	991	CTGCACCTGTGCCCCATGTGAGAGAGCCCCGTCGCGAGCCGCGTGGGACACTTTCCTGTC	1050

```

RESULT 5
US-10-188-646-12
; Sequence 12, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; NUMBER OF FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 12
; LENGTH: 1168
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (897)
US-10-188-646-12

Alignment Scores:
Score: No.: 2,13e-209
Percent Similarity: 217.00
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 70.2%
Gaps: 6

Length: 1168
Matches: 217
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
US-09-762-577B-12 (1-309) x US-10-188-646-12 (1-1168)

```

QY 1 MetC1ProLysAspSerAlaLysCysLeuHisArgG1ProClnProSerHisStrpAla 20
Db 1 ATGGGACCTTAAAGACAGTGCACAGTCTGTCGACCCCTGGACCAACAGCGGACCACTGGGCA 60

QY	2	AlaGlyAspArgIyrProThrngIngluArgCy/AGlyProAlaGserLeuGlySerProValIleu	40
Db	61	GCCGGTATAGTATCCACGACGAGAGCCCTGTGAGCCCCCGCTCTCTGGAGCCCTGTCTCTA	120
QY	41	GlyLeuAspThrTyrSarGAlaIatrPAPhHISvalAspGlyGlnIleLeuGlyGlyLeuArg	60
Db	121	GGCCTGGACACCTTCAGAGCCCTGGACCACTGTGATGGGCAAGATCTCTGGCCAGCTGGG	180
QY	61	ProleuthrGluGluGluGluGluGluGluGlyAlaGlyAlaIatHrLeuSerArgIyrProAla	80
Db	181	CCCTGGACAGAGGAGAGAGAGAGGAGGCGCGCGGGGCCACCTGTCCACAGGGGCGTGGC	240
QY	81	PheProGlyMetGlySerGluGluGluLeuAlaSerPheTyrAspTrpProLeuThr	100
Db	241	TTCCCGGCGCATGGGCTCTGAAGATTTGCTCTGGCGCTCTCTGTATGACTGGCCGCTGACT	300
QY	101	AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHISThrGlyHISGlnAsp	120
Db	301	GCTAGAGTGCACCCGAGCTGGCTGGCTGGCTCTTCCACACAGAGCCATCAGGAC	360
QY	121	LysValArgCyAspPhePheCysTyrGlyGlyLeuGlnSerTyrIyrSarGlyAspAspPro	140
Db	361	AAGGTGAGGTCTTCTTCTGCTATGGGGGCGCTGCAGAGCTGGAAGCCGCGGAGCAGACCC	420
QY	141	TrpThrGluHISAlaIatyrTrpPheProSerCyGlnPheLeuLeuAspSerIyrGlyValg	160
Db	421	TGAGCGAGAGATCCCAAGTGTATCCCAAGCTGTACTGTCTCCGTCAAAAAGAGAGA	480
QY	161	AspPheValHISserValGlnGluThrHISserGlnLeuLeuGlySerTyrPAPAspProTrp	180
Db	481	GACTTGTCCACAGTGTGCAGAGACTCACTCCACAGCTGCTGGGCTCTTGGAGCCCGTGG	540
QY	181	GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu	200
Db	541	GAAAGAACGGAGAACCCAGCCCTGTGGCCCCCTCCGCTCCGTGCTGGGTACCCCTGAG	600
QY	201	LeuProThrProArgIyrGluValGlnSerGlnSerAlaGlnGluProGly	217
Db	601	CTGCCACACCCAGAGAGAGGTCCAGTCTTAAGTGTCCAGAGAGCCAGAGA	651

```

RESULT 6
US-10-807-897-26
Sequence 26, Application US/10807897
Publication No. US20040192631A1
GENERAL INFORMATION:
APPLICANT: Xiang, Rong
APPLICANT: Zhou, He
APPLICANT: Reisfeld, Ralph A.
TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TSRI-874.1
CURRENT APPLICATION NUMBER: US/10/807,897
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ. ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 1322
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (174)...(1070)
US-10-807-897-26

```

Alignment Scores:	
Pred. No.:	2,376-209
Score:	217.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Length:	1
Matches:	2
Conservative:	0
Mismatches:	0

Query Match: 70.2% Indels: 0
DB: 8 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-807-897-26 (1-1322)

```

OY 1 MetGlyProLysAspSerAlaValCysLeuHisArgGlyProGlnProSerHisITrPAla 20
DB 174 ATGGACCTTAAGACAGTGTCCAAAGTGTCTGACACCTTGACACACCCAGCCAGCTGGGCA 233
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 224 GCCGGTGAATGGTCCACAGGAGAGCGCTGTGAGACCCGCTCTCTGGGACAGCCCTGTCTTA 293
OY 41 GlyLeuAspThrCysArgAlaITrPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 294 GGCTTGACACCTTGACAGAGCCCTGGAGCACAGTGGATGGGACAGATCTTGGGACAGCTGGCG 353
OY 61 ProLeuThrGlnGluGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
OY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 414 TTCCCGGCGATGGGCTGTGAGAGATTGCGTCTGGCTCTCTTATGACTGGGCGCTGACT 473
OY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisIThrGlyHisGlnAsp 120
DB 474 GCTGAGGTGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
OY 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 534 AAGGTGAGTGTCTTCTTCTGCTATGGGAGCTGTGACAGAGCTGAGAGAGAGAGAGAGAGAG 593
OY 141 TrpThrGlnHisAlaValTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 594 TGGACGAGCATGTCGAAGTGTGTCCCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 653
OY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 654 GACTTTGTCCACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
OY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 714 GAAGAACCGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773
OY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
DB 774 CTGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 824

```

RESULT 7

US-10-235-026-1
Sequence 1, Application US/10235026
Publication No. US20030082725A1
GENERAL INFORMATION:
APPLICANT: Deng, Gang
APPLICANT: Lin, Jiling-Huey
APPLICANT: Mosser, Michael J
TITLE OF INVENTION: DNA Encoding a No. US20030082725A1 Human Inhibitor-of-Apoptosis
FILE REFERENCE: 50972AUSD1
CURRENT APPLICATION NUMBER: US/10/235,026
PRIOR FILING DATE: 1998-07-31
PRIOR APPLICATION NUMBER: US 09/127,928
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1337
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (170)..(1066)
OTHER INFORMATION:

US-10-235-026-1

Alignment Scores:

Score: 2,398-209 Length: 1337
Percent Similarity: 217.00 Matches: 217
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
Gaps: 0

US-09-762-577B-12 (1-309) x US-10-235-026-1 (1-1337)

```

OY 1 MetGlyProLysAspSerAlaValCysLeuHisArgGlyProGlnProSerHisITrPAla 20
DB 170 ATGGACCTTAAGACAGTGTCCAAAGTGTCTGACACCTTGACACACCCAGCCAGCTGGGCA 229
OY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 230 GCCGGTGAATGGTCCACAGGAGAGCGCTGTGAGACCCGCTCTCTGGGACAGCCCTGTCTTA 289
OY 41 GlyLeuAspThrCysArgAlaITrPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 290 GGCTTGACACCTTGACAGAGCCCTGGAGCACAGTGGATGGGACAGATCTTGGGACAGCTGGCG 349
OY 61 ProLeuThrGlnGluGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 350 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 409
OY 81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 410 TTCCCGGCGATGGGCTGTGAGAGATTGCGTCTGGCTCTCTTATGACTGGGCGCTGACT 469
OY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisIThrGlyHisGlnAsp 120
DB 470 GCTGAGGTGACACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
OY 121 LysValAlaArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 530 AAGGTGAGTGTCTTCTTCTGCTATGGGAGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAG 589
OY 141 TrpThrGlnHisAlaValTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 590 TGGACGAGCATGTCGAAGTGTGTCCCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
OY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 650 GACTTTGTCCACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 709
OY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 710 GAAGAACCGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
OY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
DB 770 CTGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 820

```

RESULT 8

US-10-839-882-37
Sequence 37, Application US/10839882
Publication No. US20040203106A1
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: GUEGLER, Karl J.
APPLICANT: CORLEY, Neil C.
APPLICANT: LAB, Preeti
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
APPLICANT: JUMMING, Yang
APPLICANT: SHIH, Leo L.
TITLE OF INVENTION: PROLIFERATION AND APOPTOSIS RELATED PROTEINS

```

; FILE REFERENCE: PF-0619 PCT
; CURRENT APPLICATION NUMBER: US/10/839,882
; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US/09/807,452
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/175,737; unassigned; 60/118,559; 09/249,740; unassigned;
; 60/154,336
; PRIOR FILING DATE: 1998-10-20; 1998-10-20; 1999-02-04; 1999-04-11; 1999-04-11;
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 37
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Inycle ID No: 1520835CB1
US-10-839-882-37

```

```

Alignment Scores:
Pred. No.: 2,43e-209 Length: 1363
Score: 217.00 Matches: 217
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 70.2% Indels: 0
DB: 8 Gaps: 0

```

US-09-762-577b-12 (1-309) x US-10-839-882-37 (1-1363)

```

QY 1 MetGlyProIyAspSerAlaIyCyLeuHiaArgGlyProGlnProSerHistrAla 20
DB 215 ATGGGGCTTAAGACAGTGCACAGTGCCTGCACCGTGCACACAGCGGACCTGGGA 274
QY 21 AlaGlyAspGlyProThrGlnGluArgCyGlyProArgSerIeuGlySerProValIeu 40
DB 275 GCGGTATGATGCTCCACGACGAGCGGTGTGACCCCGCTCTGCGGACCCCTGTCTTA 334
QY 41 GlyLeuAspThrCyArgAlaItrPAspHisValAspGlyGlnIleuGlyGlnIeuArg 60
DB 335 GGCGTGAACCTGCAGAGCTGTGACACAGTGCAGATGGGACAGTCTGGGACCACTGGCG 394
QY 61 ProIeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 395 CCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 454
QY 81 PheProGlyMetGlySerGluGluGluGluGluGluGluGluGluGluGluGluGlu 100
DB 455 TTCCTGGGATGGGCTCTGAGAGGTTGCTGCTGCTGCTCTCTATGACTGGCGCTGACT 514
QY 101 AlaGluValProProGluIeuIeuAlaIaIaIaGlyPhePheHisThrGlyHisGlnAsp 120
DB 515 GCTGAGGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574
QY 121 LysValArgCyPhePheCysTyrGlyGlyIeuGlnSerTrpLysArgGlyAspAspPro 140
DB 575 AAGTGAAGTGTCTTCTTCTGCTATGAGGGGCTGACAGAGCTGGAACGGGGACCAACCC 634
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheIeuIeuArgSerIyArg 160
DB 635 TGGACGAGACATGCCAAGTGTTCCTCCAGCTGTACCTGCTCCGCTCAAAAGAGAGA 694
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnIeuIeuGlySerTrpAspProTrp 180
DB 695 GACTTTGTCCACAGTGTGAGAGACTCACTCCGAGCTGGGCTGCTGAGACCCGTGG 754
QY 181 GlnGluProGluAspAlaIaIaIaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 755 GAAGAACCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 814
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
DB 815 CTGCCACACCCAGAGAGAGAGAGAGTCCAGTCTGAAAGTGCACGAGGCCAGGA 865

```

RESULT 9

```

US-10-203-708-21
; Sequence 21, Application US/10203708
; Publication No. US20030149238A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GSP0013
; CURRENT APPLICATION NUMBER: US/10/203,708
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-708-21

```

```

Alignment Scores:
Pred. No.: 6,21e-169 Length: 1068
Score: 177.00 Matches: 177
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 57.3% Indels: 0
DB: 6 Gaps: 0

```

US-09-762-577b-12 (1-309) x US-10-203-708-21 (1-1068)

```

QY 1 MetGlyProIyAspSerAlaIyCyLeuHiaArgGlyProGlnProSerHistrAla 20
DB 1 ATGGGACCTTAAGACAGTGCACAGTGCCTGCACCGTGCACACAGCGGACCTGGGA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCyGlyProArgSerIeuGlySerProValIeu 40
DB 61 GCGGTATGATGCTCCACGACGAGAGCGCTGTGACCCCGCTCTGAGGAGCCCTGTCTTA 120
QY 61 GlyLeuAspThrCyArgAlaItrPAspHisValAspGlyGlnIleuGlyGlnIeuArg 60
DB 121 GGCGTGAACCTGCAGAGCTGTGACACAGTGCAGATGGGACAGTCTGGGACCACTGGCG 180
QY 81 PheProGlyMetGlySerGluGluGluGluGluGluGluGluGluGluGluGluGlu 100
DB 61 ProIeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 181 CCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 81 PheProGlyMetGlySerGluGluGluGluGluGluGluGluGluGluGluGluGlu 100
DB 241 TTCCTGGGATGGGCTCTGAGAGGTTGCTGCTGCTGCTCTCTATGACTGGCGCTGACT 300
QY 101 AlaGluValProProGluIeuIeuAlaIaIaIaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTGAGGTGCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 121 LysValArgCyPhePheCysTyrGlyGlyIeuGlnSerTrpLysArgGlyAspAspPro 140
DB 361 AAGTGAAGTGTCTTCTTCTGCTATGAGGGGCTGACAGAGCTGGAACGGGGACCAACCC 420
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheIeuIeuArgSerIyArg 160
DB 421 TGGACGAGACATGCCAAGTGTTCCTCCAGCTGTCACTGCTCCGCTCAAAAGAGAGA 480
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnIeuIeuGlySerTrp 177
DB 481 GACTTTGTCCACAGTGTGAGAGACTCACTCCAGCTGTGGGCTGCTGG 531

```

RESULT 10

```
US-10-723-860-4697
; Sequence 4697, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent version 3.2
; SEQ ID NO 4697
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-4697

Alignment Scores:
Pred. No.: 6,676-141 Length: 449
Score: 149.00 Matches: 149
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 48.2% Indels: 0
DB: 8 Gaps: 0

US-09-762-577B-12 (1-309) X US-10-723-860-4697 (1-449)

QY 1 MetGlyProLyAspSerAlaLySCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGACCTAAAGACAGTGCCTGACCTGACCTGACCAACAGCCAGCCACTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCGGTGATGGTCCACAGCAGAGCGCTGTGACCCCTCTCTGGGAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
DB 121 GGCCTGACACCTGACAGACCTGGGACCACTGATGGGACATCTTGGCCAGCTGGCG 180
QY 61 ProLeuThrGlnGluGlnGluGlnGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
DB 181 CCCCTGACAGAGAGAGAGAGAGAGAGGCGCGCGGCGCACCTTGTCCAGGGGGCTGCC 240
QY 81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 241 TTCCCGGCAATGGGCTGTGAGAGTGGTGTGGCTCTCTTATGACTGGCCGCTGACT 300
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTAGAGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTTCTTCCACAGGCCATCAGAC 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLyAspArgGlyAspAspPro 140
DB 361 AAGGTGAGGTCTTCTTCTGCTATGGGGCGCTGACAGCTGGAAGCGGGGAGACGACCCC 420
QY 141 TrpThrGlnHisAlaValSerTrpPhePro 149
DB 421 TGGACGGAGCATGCGCAAGTGTTCCTCC 447

RESULT 11
US-10-203-708-22
; Sequence 22, Application US/10203708
; Publication No. US20030149238A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; APPLICANT: SmithKline Beecham P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
```

```
CURRENT APPLICATION NUMBER: US/10/203,708
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-708-22

Alignment Scores:
Pred. No.: 1,056-140 Length: 769
Score: 149.00 Matches: 149
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 48.2% Indels: 0
DB: 6 Gaps: 0

US-09-762-577B-12 (1-309) X US-10-203-708-22 (1-769)

QY 1 MetGlyProLyAspSerAlaLySCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 1 ATGGACCTAAAGACAGTGCCTGACCTGACCTGACCAACAGCCAGCCACTGGGCA 60
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 61 GCGGTGATGGTCCACAGCAGAGCGCTGTGACCCCTCTCTGGGAGCCCTGTCTTA 120
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
DB 121 GGCCTGACACCTGACAGACCTGGGACCACTGATGGGACATCTTGGCCAGCTGGCG 180
QY 61 ProLeuThrGlnGluGlnGluGlnGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
DB 181 CCCCTGACAGAGAGAGAGAGAGAGGCGCGCGGCGCACCTTGTCCAGGGGGCTGCC 240
QY 81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
DB 241 TTCCCGGCAATGGGCTGTGAGAGTGGTGTGGCTCTCTTATGACTGGCCGCTGACT 300
QY 101 AlaGluValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 301 GCTAGAGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTTCTTCCACAGGCCATCAGAC 360
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLyAspArgGlyAspAspPro 140
DB 361 AAGGTGAGGTCTTCTTCTGCTATGGGGCGCTGACAGCTGGAAGCGGGGAGACGACCCC 420
QY 141 TrpThrGlnHisAlaValSerTrpPhePro 149
DB 421 TGGACGGAGCATGCGCAAGTGTTCCTCC 447

RESULT 12
US-10-723-860-8265
; Sequence 8265, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
```

```
/ NUMBER OF SEQ ID NOS: 8393
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 8265
/ LENGTH: 858
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-723-860-8265

Alignment Scores:
Pred. No.: 1,93e-122      Length: 858
Score: 131.00           Matches: 131
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 42.4%           Indels: 0
DB: 8                      Gaps: 0

US-09-762-577B-12 (1-309) x US-10-723-860-8265 (1-858)

QY 150 SerCysGlnPheLeuLeuArgSerLysGlyArgAspPheValHisSerValGlnGlnThr 169
Db 193 AGCTGTCAAGTTCCTGCTCCGGTCAAAAGAGAACTTTGTCCACAGTGTGCGAGAGACT 252
QY 170 HisSerGlnLeuLeuGlySerTTPAspProTTPGlnGlnProGlnAspAlaAlaProVal 189
Db 253 CACTCCAGCTGTGGGCTCCTGGACCCGTTGGAGAACCGGAAGACGACCCCTGTG 312
QY 190 AlaProSerValProAlaSerGlyTyrProGlnLeuProThrProArgArgGlnValGln 209
Db 313 GCCCCTCCGCTCTGCTCTGGTACCTGAGCTGCCACCCAGAGAGAGAGAGAGAGAGAG 372
QY 210 SerGlnSerAlaGlnGlnProGlyAlaArgAspValGlnGlnLeuArgArgLeuGln 229
Db 373 TCTGAAAGTGGCCAGGAGCCAGGAGGATGTGGAGGCGAGCTGGCGGCGCTGCAG 432
QY 230 GlnGlnArgThrCysLysValCysLeuAspArgAlaValSerIleValPheValProCys 249
Db 433 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
QY 250 GlyHisLeuValCysAlaGlnCysAlaProGlyLeuGlnLeuCysProIleCysArgAla 269
Db 493 GGGCACCCTGCTGTGTGTGAGTGTGCCCCGGCGCTGCACATCTTTGTGCGCTGC 552
QY 270 ProValArgSerArgValArgThrPheLeuSer 280
Db 553 CCGGTCCGACGCGCGGCGACACTTCTGTCTCC 585

RESULT 13
US-10-450-763-27354
/ Sequence 27354, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ PRIOR FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO: 27354
/ LENGTH: 614
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: SIMILAR
/ LOCATION: (309) (614)
/ OTHER INFORMATION: 358 homologous to Homo sapiens inhibitor of apoptosis protein
/ OTHER INFORMATION: KIAA, accession number AF301009, Smith-Waterman Score=86.
```

```
US-10-450-763-27354

Alignment Scores:
Pred. No.: 1,99e-111      Length: 614
Score: 120.00           Matches: 120
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 38.8%           Indels: 0
DB: 9                      Gaps: 0

US-09-762-577B-12 (1-309) x US-10-450-763-27354 (1-614)

QY 98 ProLeuThrAlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGly 117
Db 26 CCGTGAAGTCTGAGGTGCCACCCGAGCTGTGCTCTCCGGCTTCTTCCACACAGGC 85
QY 118 HisGlnAspLysValAlaArgCysPhePheCysTyrGlyGlnGlnSerTTPValArgGly 137
Db 86 CATCAGACAAAGTAGAGTGTCTTCTGTATGGGGCCCTGCAGAGCTGGAAGCGCGG 145
QY 138 AspAspProTTPThrGlnHisAlaLysTTPPheProSerCysGlnPheLeuLeuArgSer 157
Db 146 GACGACCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 205
QY 158 LysGlyArgAspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTTP 177
Db 206 AAAGAGAGAGACTTTGTCCACAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAG 265
QY 178 AspProTTPGlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGly 197
Db 266 GACCCGTGGAGAAAGCCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 325
QY 198 TyrProGlnLeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGly 217
Db 326 TACCTGAGCTGCCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 385

RESULT 14
US-10-296-115-63
/ Sequence 63, Application US/10296115
/ Publication No. US20040053248A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides
/ FILE REFERENCE: 784PCT
/ CURRENT APPLICATION NUMBER: US/10/296,115
/ PRIOR FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: US09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ NUMBER OF SEQ ID NOS: 1478
/ SEQ ID NO: 63
/ LENGTH: 615
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-296-115-63

Alignment Scores:
Pred. No.: 1,99e-111      Length: 615
Score: 120.00           Matches: 120
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 38.8%           Indels: 0
DB: 7                      Gaps: 0

US-09-762-577B-12 (1-309) x US-10-296-115-63 (1-615)

QY 98 ProLeuThrAlaGlnValProProGlnLeuLeuAlaAlaGlyPhePheHisThrGly 117
Db 27 CCGTGAAGTCTGAGGTGCCACCCGAGCTGTGCTCTCCGGCTTCTTCCACACAGGC 86
QY 118 HisGlnAspLysValAlaArgCysPhePheCysTyrGlyGlnGlnSerTTPValArgGly 137
```

Db 87 CATCAGACAGAGTGGTGGCTTCTTCTGATATGGGGGCTGCAGAGCTGGAAGGCGGG 146

Job time : 631 secs

Qy 138 AspAspProTTPThGlnHisAlaIysTrpPheProSerCysGlnPheLeuLeuArgSer 157
Db 147 GACGACCCCTGACGAGCATGCTCAAGTGGTTCCCGACGTCTCAGTCTCTGCTCCGCTCA 206

Qy 158 LysGlyArgAspPheValHisSerValGlnGlnTrpHisSerGlnLeuLeuGlySerTrp 177
Db 207 AAAGAGAGACTTGTGTCCAGCTGTGCAAGAGACTCTCCAGCTGCTGGCTTTGG 266

Qy 178 AspProTTPGluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGly 197
Db 267 GACCCGTGGGAAGAACCGGAAGACCGACCCCTGTGGCCCTCCCTGCTGCTGCTGG 326

Qy 198 TyrProGluLeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGly 217
Db 327 TACCTGAGCTGCCACACAGAGAGAGAGGTCCAGTCTGAAGTGCACAGAGCCAGGA 386

RESULT 15

US-10-188-646-11

/ Sequence 11, Application US/10188646
/ Publication No. US2004005565A1

/ GENERAL INFORMATION:

/ APPLICANT: C. Frank Bennett

/ TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION

/ FILE REFERENCE: RTS-0373

/ CURRENT APPLICATION NUMBER: US/10/188,646

/ CURRENT FILING DATE: 2002-07-02

/ NUMBER OF SEQ ID NOS: 153

/ SEQ ID NO 11

/ LENGTH: 4810

/ TYPE: DNA

/ ORGANISM: H. sapiens

/ FEATURE:

US-10-188-646-11

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-762-577b-12 (1-309) x US-10-188-646-11 (1-4810)

Qy 1 MetGlyProLysAspSerAlaIysCysLeuHisArgGlyProGlnProSerHisTrpAla 20

Db 310 ATGGGACCTTAAGAGACAGTCCAGAGTGCCTGCACTGGACCAAGCCGAGCCACTGGGCA 369

Qy 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40

Db 370 GCCGGTGTATGTCTCCAGCAGAGAGGCGCTGTGACCCCGCTCTCTGGGCAAGCCCTGCTTA 429

Qy 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60

Db 430 GGCTGTGACACTGTGAGAGCTGTGGACCACTGTGATGGGAGATCTTGGCCAGCTGGCG 489

Qy 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80

Db 490 CCCCTGACAG 549

Qy 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100

Db 550 TTCCCGGCGATGGGCTGTGAGAGTGTGCTGTGGCTCTCTTAATGACTGGCCGCTGACT 609

Qy 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGly 117

Db 610 GCTAGGTGACCAAG 660

Search completed: April 24, 2006, 10:13:42

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2006, 10:13:58 ; Search time 1852 Seconds
(without alignments)
675.163 Million cell updates/sec

Title: US-09-762-577b-12
Perfect score: 309
Sequence: 1 MGPDSAKCXHRGPQPSHWA.....GLQSGLPAPLCLEMTVFWMAC 309

Searching tables: **OLIGO**
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 9288580 seqs, 2023302648 residues

Word sizes: **1**

Total number of hits satisfying chosen parameters: 18575175

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=x1h
-Q=/abs/ABSSWEB.spool/US09762577/runat_24042006_105939_1250/app_query.fasta_1
-DB=published.Applications NA New -QFMT=fastap -SUFFIX=p2nol1.rnpbn
-MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs806h
-USER=US09762577@cgc 1.1 545 @runat_24042006_105939_1250 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DRV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database: Published Applications NA New:*

1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/ECT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	177	57.3	1068 14	US-11-135-855-21 Sequence 21, Appl
2	149	48.2	769 14	US-11-135-855-22 Sequence 22, Appl

3	14	4.5	3076	7	US-10-960-414-432	Sequence 432, App
4	14	4.5	3837	14	US-11-136-527-2596	Sequence 2596, Ap
5	10	3.2	600	14	US-11-136-527-6853	Sequence 6853, Ap
6	10	3.2	1257	9	US-10-301-480-39825	Sequence 39825, A
7	10	3.2	1257	10	US-10-301-480-653234	Sequence 653234, A
8	10	3.2	2106	14	US-11-136-527-2757	Sequence 2757, Ap
9	10	3.2	2468	14	US-11-136-527-303	Sequence 303, App
10	9	2.9	201	8	US-10-995-561-63908	Sequence 63908, A
11	9	2.9	201	8	US-10-995-561-64173	Sequence 64173, A
12	9	2.9	599	14	US-11-128-061-1885	Sequence 1885, Ap
13	9	2.9	599	14	US-11-128-061-5527	Sequence 5527, Ap
14	9	2.9	599	14	US-11-128-049-1885	Sequence 1885, Ap
15	9	2.9	599	14	US-11-128-049-5527	Sequence 5527, Ap
16	9	2.9	1659	8	US-10-775-169-1	Sequence 7, Appl1
17	9	2.9	70513	8	US-10-995-561-13368	Sequence 13368, A
18	9	2.9	191343	14	US-11-112-908-53	Sequence 53, Appl
19	8	2.6	25	14	US-11-121-849-61904	Sequence 61904, A
20	8	2.6	25	14	US-11-121-849-61905	Sequence 61905, A
21	8	2.6	25	14	US-11-121-849-61906	Sequence 61906, A
22	8	2.6	25	14	US-11-121-849-61914	Sequence 61914, A
23	8	2.6	201	8	US-10-995-561-64234	Sequence 64234, A
24	8	2.6	490	11	US-11-096-568A-14006	Sequence 14006, A
25	8	2.6	494	6	US-09-925-065A-930869	Sequence 930869, A
26	8	2.6	515	6	US-09-925-065A-701445	Sequence 701445, A
27	8	2.6	532	6	US-09-925-065A-933631	Sequence 933631, A
28	8	2.6	532	6	US-09-925-065A-952117	Sequence 952117, A
29	8	2.6	557	6	US-09-925-065A-504456	Sequence 504456, A
30	8	2.6	557	6	US-09-925-065A-504457	Sequence 504457, A
31	8	2.6	557	6	US-09-925-065A-504459	Sequence 504459, A
32	8	2.6	560	6	US-09-925-065A-212847	Sequence 212847, A
33	8	2.6	560	10	US-10-301-480-299879	Sequence 299879, A
34	8	2.6	560	10	US-10-301-480-913288	Sequence 913288, A
35	8	2.6	572	9	US-10-301-480-15338	Sequence 15338, A
36	8	2.6	572	10	US-10-301-480-628747	Sequence 628747, A
37	8	2.6	576	10	US-10-301-480-477677	Sequence 477677, A
38	8	2.6	576	10	US-10-301-480-1091066	Sequence 1091066, A
39	8	2.6	578	6	US-09-925-065A-411472	Sequence 411472, A
40	8	2.6	587	6	US-09-925-065A-389545	Sequence 389545, A
41	8	2.6	588	6	US-09-925-065A-191034	Sequence 191034, A
42	8	2.6	590	6	US-09-925-065A-658830	Sequence 658830, A
43	8	2.6	593	10	US-10-301-480-597990	Sequence 597990, A
44	8	2.6	593	10	US-10-301-480-1211399	Sequence 1211399, A
45	8	2.6	598	10	US-10-301-480-457909	Sequence 457909, A

ALIGNMENTS

RESULT 1
US-11-135-855-21
Sequence 21, Application US/11135855
Publication No. US2005025557A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPO5013
CURRENT APPLICATION NUMBER: US/11/135, 855
PRIOR FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/10/203, 708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182, 172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186, 084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 1068
TYPE: DNA
ORGANISM: Homo sapiens
US-11-135-855-21

Alignment Scores:

Pred. No.: 2,91e-160 Length: 1068
 Score: 177.00 Matches: 177
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 57.3% Indels: 0
 DB: 14 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-135-855-21 (1-1068)

```

QY      1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB      1 ATGGACCTAAAGACAGTGCAGAGTGCCTGGACACCGTGGACACAGCGGACCTGGGCA 60
QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB      61 GCCGTGATGATGCCACGACGAGAGCGCTGTGACCCCGCTCTCTGGGCAAGCCCTGTCTTA 120
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB      121 GGCTGGACACCTGCACAGCCTGGGACCACTGGATGGGCAATCCTGGGCGACGCTGGCG 180
QY      61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB      181 CCCCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY      81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheThrAspTrpProLeuThr 100
DB      241 TTCCCGGCAATGGGCTGTGAGAGTTCGCTGCTGCTCTCTCTATACCTGGCGCTGACT 300
QY      101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB      301 GCTGAGGTGCGACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY      121 LysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB      361 AAGGTGAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
QY      141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB      421 TGGACGAGCATGCCAAGTGTTCCTCCAGCTGCACTTCTCTCGGTCACAAAAGAAAGA 480
QY      161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrp 177
DB      481 GACTTGTCCACAGTGTGACAGAGACTCTCCAGCTGCTGGGCTCTCTGG 531

```

RESULT 2

US-11-135-855-22
 ; Sequence 22, Application US/11135855
 ; Publication No. US2005025557A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SMITHKLINE BEECHAM CORPORATION
 ; APPLICANT: SMITHKLINE BEECHAM P.1.C.
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GFS0013
 ; CURRENT APPLICATION NUMBER: US/11/135,855
 ; CURRENT FILING DATE: 2005-05-24
 ; PRIOR APPLICATION NUMBER: US/10/203,708
 ; PRIOR FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: PCT/US01/04703
 ; PRIOR FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: 60/182,172
 ; PRIOR FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: 60/186,084
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FaSTSeq for Windows Version 3.0
 ; SEQ ID NO 22
 ; TYPE: DNA
 ; LENGTH: 769
 ; INDELS: 0
 ; ORGANISM: Homo sapiens
 ; US-11-135-855-22

Alignment Scores:

Pred. No.: 2,04e-133 Length: 769
 Score: 149.00 Matches: 149
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 48.2% Indels: 0
 DB: 14 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-135-855-22 (1-769)

```

QY      1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB      1 ATGGACCTAAAGACAGTGCAGAGTGCCTGGACACCGTGGACACAGCGGACCTGGGCA 60
QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB      61 GCCGTGATGATGCCACGACGAGAGCGCTGTGACCCCGCTCTCTGGGCAAGCCCTGTCTTA 120
QY      41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB      121 GGCTGGACACCTGCACAGCCTGGGACCACTGGATGGGCAATCCTGGGCGACGCTGGCG 180
QY      61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB      181 CCCCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY      81 PheProGlyMetGlySerGlnGluLeuArgLeuAlaSerPheThrAspTrpProLeuThr 100
DB      241 TTCCCGGCAATGGGCTGTGAGAGTTCGCTGCTGCTCTCTCTATACCTGGCGCTGACT 300
QY      101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB      301 GCTGAGGTGCGACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY      121 LysValArgCysPhePheCysTyrglyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB      361 AAGGTGAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
QY      141 TrpThrGlnHisAlaLysTrpPhePro 149
DB      421 TGGACGAGCATGCCAAGTGTTCCTCCAGCTGCACTTCTCTCGGTCACAAAAGAAAGA 447

```

RESULT 3

US-10-960-414-432
 ; Sequence 432, Application US/10960414
 ; Publication No. US20060074565A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MILLER, LANCE D.
 ; APPLICANT: GEORGE, JOSH
 ; APPLICANT: VEGA, VINCENTIUS B.
 ; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
 ; PROGNOSIS, AND DIAGNOSIS OF CANCERS
 ; FILE REFERENCE: 38271-76067
 ; CURRENT APPLICATION NUMBER: US/10/960,414
 ; CURRENT FILING DATE: 2004-10-06
 ; NUMBER OF SEQ ID NOS: 500
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 432
 ; LENGTH: 3076
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-960-414-432

Alignment Scores:

Pred. No.: 0.00779 Length: 3076
 Score: 14.00 Matches: 14
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 4.5% Indels: 0
 DB: 7 Gaps: 0

US-09-762-577b-12 (1-309) x US-10-960-414-432 (1-3076)


```
US-11-128-061-1885
; Sequence 1885, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128.061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1885
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(71)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-1885

Alignment Scores:
Pred. No.: 119 Length: 599
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.9% Indels: 0
DB: 14 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-128-061-1885 (1-599)
QY 245 ValpheValProCysGlyHisLeuVal 253
Db 163 GTTTTGTCTCTGTGTGACATCTGTC 189

RESULT 13
US-11-128-061-5527
; Sequence 5527, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128.061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5527
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (26)..(71)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-5527

Alignment Scores:
Pred. No.: 119 Length: 599
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.9% Indels: 0
DB: 14 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-128-061-5527 (1-599)
QY 245 ValpheValProCysGlyHisLeuVal 253
Db 163 GTTTTGTCTCTGTGTGACATCTGTC 189

RESULT 14
US-11-128-049-1885
; Sequence 1885, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128.049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1885
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(71)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-1885

Alignment Scores:
Pred. No.: 119 Length: 599
Score: 9.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 2.9% Indels: 0
DB: 14 Gaps: 0

US-09-762-577b-12 (1-309) x US-11-128-049-1885 (1-599)
QY 245 ValpheValProCysGlyHisLeuVal 253
Db 163 GTTTTGTCTCTGTGTGACATCTGTC 189

RESULT 15
US-11-128-049-5527
; Sequence 5527, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
```

```

; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5527
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(71)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-5527

```

```

Alignment Scores:
Pred. No.:      119      Length:      599
Score:          9.00     Matches:      9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:      2.9%   Indels:      0
DB:               14     Gaps:      0

```

US-09-762-577B-12 (1-309) x US-11-128-049-5527 (1-599)

```

Qy      245 ValPheValProCysGlyHisLeuVal 253
Db      163 GTTTTGTCTCTGTGACATCTGTC 189

```

Search completed: April 24, 2006, 10:45:06
Job time : 1858 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocelebration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2006, 09:59:54 ; Search time 6648 Seconds

(without alignments)
2569.961 Million cell updates/sec

Title: US-09-762-577B-12
Perfect score: 309
Sequence: 1 MGPRDSAKCLHRGPQSHWA.....GLQSGLPAPLCLFTVTFWAC 309

Searching values: **OLIGO**
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 79147668 segs, 27645789525 residues

Word sizes: **1**

Total number of hits satisfying chosen parameters: 158263852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+.p2n.model -DEV=xlp
-O=/abs/ABSSWEB.spool/US09762577/runat 24042006 105932 1105/app.query.fasta_1
-DB=Pending Patents NA Main -OFT=fastcap -SUFFIX=p2nol1.rmp -MIMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs03p
-USER=US09762577 @CGN 1 1 11077 @runat 24042006 105932 1105 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=60 -Fgapext=7
-Ygapop=60 -Ygapext=60 -Delop=60 -Delext=60

Database :

Pending Patents NA Main:*

1: /cgn2_6/prodata/1/pna/PCTUSA_COMB.seq:*

2: /cgn2_6/prodata/1/pna/PCTUSB_COMB.seq:*

3: /cgn2_6/prodata/1/pna/PCTUSC_COMB.seq:*

4: /cgn2_6/prodata/1/pna/US06_COMB.seq:*

5: /cgn2_6/prodata/1/pna/US075_COMB.seq:*

6: /cgn2_6/prodata/1/pna/US076_COMB.seq:*

7: /cgn2_6/prodata/1/pna/US077_COMB.seq:*

8: /cgn2_6/prodata/1/pna/US078_COMB.seq:*

9: /cgn2_6/prodata/1/pna/US079_COMB.seq:*

10: /cgn2_6/prodata/1/pna/US080_COMB.seq:*

11: /cgn2_6/prodata/1/pna/US081_COMB.seq:*

12: /cgn2_6/prodata/1/pna/US082_COMB.seq:*

13: /cgn2_6/prodata/1/pna/US083_COMB.seq:*

14: /cgn2_6/prodata/1/pna/US084_COMB.seq:*

15: /cgn2_6/prodata/1/pna/US085_COMB.seq:*

16: /cgn2_6/prodata/1/pna/US086_COMB.seq:*

17: /cgn2_6/prodata/1/pna/US087_COMB.seq:*

18: /cgn2_6/prodata/1/pna/US088_COMB.seq:*

19: /cgn2_6/prodata/1/pna/US089_COMB.seq:*

20: /cgn2_6/prodata/1/pna/US090_COMB.seq:*

21: /cgn2_6/prodata/1/pna/US091_COMB.seq:*

22: /cgn2_6/prodata/1/pna/US092_COMB.seq:*

23: /cgn2_6/prodata/1/pna/US093_COMB.seq:*

24: /cgn2_6/prodata/1/pna/US094_COMB.seq:*

25: /cgn2_6/prodata/1/pna/US095A_COMB.seq:*

26: /cgn2_6/prodata/1/pna/US095B_COMB.seq:*

27: /cgn2_6/prodata/1/pna/US095C_COMB.seq:*

Result No.	Score	Query Match	Length	DB ID	Description
1	280	90.6	843	27	US-09-594-119-2
2	280	90.6	843	43	US-10-244-586-2
3	280	90.6	1246	3	PCT-US99-1738-11
4	280	90.6	1260	1	PCT-US03-20821-4
5	280	90.6	1260	42	US-10-170-235-27143
6	280	90.6	1260	42	US-10-188-646-4
7	280	90.6	1260	52	US-10-553-355-11

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

```

8      280      90.6      1260      63      US-10-940-774-1949      Sequence 1949, Ap
9      280      90.6      1260      64      US-10-940-774-1949      Sequence 1949, Ap
10     280      90.6      1268      1      PCT-US02-29560-182      Sequence 182, Ap
11     280      90.6      1268      1      PCT-US02-29560A-182      Sequence 182, Ap
12     280      90.6      1268      43      US-10-245-882-182      Sequence 182, Ap
13     280      90.6      1268      43      US-10-245-882-182      Sequence 182, Ap
14     280      90.6      1268      62      US-10-807-897-28      Sequence 1181, Ap
15     280      90.6      1268      82      US-60-685-372-1181      Sequence 1181, Ap
16     280      90.6      1376      27      US-09-594-119-11      Sequence 1130, Ap
17     280      90.6      1376      27      US-09-594-119-11      Sequence 1130, Ap
18     280      90.6      982      77      US-60-278-258-117511      Sequence 45583, A
19     217      70.2      897      3      PCT-US05-22501-1130      Sequence 17511, A
20     217      70.2      897      82      US-60-680-473-45583      Sequence 45583, A
21     217      70.2      1168      1      PCT-US03-20821-12      Sequence 12, Ap
22     217      70.2      1168      42      US-10-188-646-12      Sequence 12, Ap
23     217      70.2      1168      52      US-10-553-355-10      Sequence 10, Ap
24     217      70.2      1332      1      PCT-US02-29560-181      Sequence 181, Ap
25     217      70.2      1332      1      PCT-US02-29560A-181      Sequence 181, Ap
26     217      70.2      1332      3      PCT-US04-08932-26      Sequence 26, Ap
27     217      70.2      1332      43      US-10-245-882-181      Sequence 181, Ap
28     217      70.2      1332      62      US-10-807-897-26      Sequence 26, Ap
29     217      70.2      1332      82      US-60-685-372-1183      Sequence 1183, Ap
30     217      70.2      1337      43      US-10-235-026-11      Sequence 1, Ap
31     217      70.2      1337      43      US-10-235-026-11      Sequence 1, Ap
32     217      70.2      1363      22      US-09-296-904-7       Sequence 7, Ap
33     217      70.2      1363      33      US-09-807-452-37      Sequence 37, Ap
34     217      70.2      1363      62      US-10-839-882-37      Sequence 37, Ap
35     177      57.3      1068      1      PCT-US01-04703-21      Sequence 21, Ap
36     177      57.3      1068      43      US-10-203-708-21      Sequence 21, Ap
37     177      57.3      1068      71      US-11-135-855-21      Sequence 21, Ap
38     150      48.5      1364      75      US-60-172-373-13322      Sequence 13322, A
39     149      48.2      449      2      PCT-US03-38193-4697      Sequence 4697, Ap
40     149      48.2      449      61      US-10-723-860-4697      Sequence 4697, Ap
41     149      48.2      769      1      PCT-US01-04703-22      Sequence 22, Ap
42     149      48.2      769      43      US-10-203-708-22      Sequence 22, Ap
43     149      48.2      769      71      US-11-135-855-22      Sequence 22, Ap
44     145      46.9      462      24      US-09-471-275-9645      Sequence 9645, Ap
45     145      46.9      462      48      US-10-302-689A-68288      Sequence 68288, A

```

ALIGNMENTS

```

RESULT 1
US-09-594-119-2
/ Sequence 2, Application US/09594119
/ GENERAL INFORMATION:
/ APPLICANT: GOMES, BRUCE C.
/ APPLICANT: KASOF, GARRETT M.
/ APPLICANT: PROSSER, JUDITH C.
/ TITLE OF INVENTION: NOVEL PROTEIN
/ FILE REFERENCE: DJB/009901/0270799
/ CURRENT FILING DATE: 2000-06-14
/ PRIOR APPLICATION NUMBER: US/09/594,119
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 843
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-594-119-2

Alignment Scores:
Pred. No.:      2,94e-266
Score:          280.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match:    90.6%
DB:             27

```

US-09-762-577b-12 (1-309) x US-09-594-119-2 (1-843)

```

QY      1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
1      1 ARGGAGCACTAAAGACAGAGCCCAAGCTGCTGACCCGTGAGCCAGACCGAGCACTGGGCA 60
QY      21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
61      61 GCCGTGTGATGGTCCACGACGAGAGCGGTGTGAGCCCGCTCTGTGGGAGCCGTGCTTA 120
QY      41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnLeuGlnLeuArg 60
121      121 GGCTGGACACCTGACAGAGCTGGAGCCACCTGATGGAGTGGCAGATCTGGGCGACCTGG 180
QY      61 ProLeuThrGlnGluGlnGluGlnGluValAlaGlyAlaThrLeuSerArgGlyProAla 80
181      181 CCCCTGACAGAGGAGAAAGAGAGAGAGGCGCGGGGCGACCTGTCTCAGGGGGCTGGCC 240
QY      81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
241      241 TTCCCGGCGATGGGCTGTGAGAGAGTTCGTGACCTCTCTATGACTGGCGGCTGACT 300
QY      101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
301      301 GCTAGAGTGCACCCGAGAGCTGCTGGCTGCGGCTTCTTCCACAGAGCCATCAGAGAC 360
QY      121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
361      361 AAGGTAGGTGCTCTCTCTGCTATGAGGGGCTGACGAGCTGAAAGCGCGGAGAGACCCC 420
QY      141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
421      421 TGGACGAGACATGCGCAAGTGTCTCCAGCTGTCACTCTGCTCGGCTGAAAAAGAGA 480
QY      161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
481      481 GACTTGTCCACAGTGTGAGAGAGACTCCTCCAGCTGTGGGCTCTTGGACCCGTGG 540
QY      181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
541      541 GAAGAACCGAAGACGAGCGCCCTGTGGCCCTCTGCTCTGCTGCTGCTGCTGCTGAG 600
QY      201 LeuProThrProArgArgGluValGlnSerGlySerAlaGlnGluProGluAlaAspAsp 220
601      601 CTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTCCCAAGAGCCAGAGCCAGAGAT 660
QY      221 ValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysLysValCysLeuAspArg 240
661      661 GTGAGGCGGAGCGTGGCGCGCTGCGAGAGAGAGACGTCAGAGGTGTGCTGGACCGC 720
QY      241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
721      721 GCCGTGTCCATCTGCTTGTGCGGTGGCGACCTGCTGTGCTAGTGTGCTGCTGCTGCTG 780
QY      261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
781      781 CTGAGAGTGTGCCCATCTGACAGAGCCCGGTGCCAGCGCGGTGGCACTTCTCTGTCC 840
Db

RESULT 2
US-10-244-586-2
/ Sequence 2, Application US/10244586
/ GENERAL INFORMATION:
/ APPLICANT: GOMES, BRUCE C.
/ APPLICANT: KASOF, GARRETT M.
/ APPLICANT: PROSSER, JUDITH C.
/ TITLE OF INVENTION: NOVEL PROTEIN
/ FILE REFERENCE: DJB/009901/0270799
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US/09/594,119
/ PRIOR FILING DATE: 2000-06-14
/ PRIOR APPLICATION NUMBER: 60/139,291
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1

```



```
; SEQ ID NO 2
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-586-2

Alignment Scores:
Pred. No.: 2,94e-266 Length: 843
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 43 Gaps: 0

US-09-762-577b-12 (1-309) x US-10-244-586-2 (1-843)

OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisIstRpAla 20
Db 1 ATGGGACCTAAAGACAGTGCACCAAGTGCCTGCACCTGGACCAACCCGAGCCACTGGGCA 60
OY 21 AlaGlyAspGlyProThrGlnGlnLysArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 61 GCGGTGATGTGTCCACCCAGAGCGCTGTGGACCCCTCTGTGGCAGCCCTGTCTTA 120
OY 41 GlyLeuAspThrCysArgAlaIstRpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 121 GGCTGGACACCTGCAGAGCCTGGGACCACTGGATGGGACAGATCTGGGCCAGCTGGCG 180
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 181 CCCCTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
OY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyraPstProLeuThr 100
Db 241 TTCCCGGACATGGGCTGTGAGAGATGGGCTGTGGCTCTCTTAAGACTGGCGCTGACT 300
OY 101 AlaGlnValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 301 GCTGAGGTGCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 360
OY 121 LysValAlaArgCysPhePheCysTyrglyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db 361 AAGGTGAGTGTCTTCTGTGATGGGGGCTGCAGAGCTGGAGCGGGGAGACACACCC 420
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerIstRpArg 160
Db 421 TGGACGGAGCATGCCAAGTGGTCCCGCAGCTGTCTGTCTGTCTGTCTGTCTGTCTGT 480
OY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlnGlnGlnGlnGlnGln 180
Db 481 GACTTTGTCCACAGTGTGCAGAGACTCACTCCAGCTGTGGGCTCTGGAGACCCGTGG 540
OY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyraProGln 200
Db 541 GAAGAACCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
OY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyValaArgAsp 220
Db 601 CTGCCCAACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
OY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 661 GTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
OY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db 721 GCCGTGTCCATGCTTTGTGCGCGGTGGCCACCTGTGTGTGTGTGTGTGTGTGTGTGT 780
OY 261 LeuGlnLeuCysProIleCysArgAlaProValaArgSerArgValaArgThrPheLeuSer 280
Db 781 CTGAGAGTGTGCCCATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
RESULT 3
```

```
PCT-US99-17738-11
; Sequence 11, Application PC/TUS9917738
; GENERAL INFORMATION:
; APPLICANT: Dranooff, Glenn
; APPLICANT: Schmolinger, Jan
; APPLICANT: Hodi, F. Stephen
; APPLICANT: Molllick, Joseph
; TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
; FILE REFERENCE: 50059/005W02
; CURRENT APPLICATION NUMBER: PCT/US99/17738
; EARLIER FILING DATE: 1999-06-06
; EARLIER APPLICATION NUMBER: 60/095,766
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-17738-11

Alignment Scores:
Pred. No.: 4,21e-266 Length: 1246
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 3 Gaps: 0

US-09-762-577b-12 (1-309) x PCT-US99-17738-11 (1-1246)

OY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisIstRpAla 20
Db 160 ATGGGACCTAAAGACAGTGCACCAAGTGCCTGCACCTGGACCAACCCGAGCCACTGGGCA 219
OY 21 AlaGlyAspGlyProThrGlnGlnLysArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 220 GCGGTGATGTGTCCACCCAGAGCGCTGTGGACCCCTCTGTGGCAGCCCTGTCTTA 279
OY 41 GlyLeuAspThrCysArgAlaIstRpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 280 GGCTGGACACCTGCAGAGCCTGGGACCACTGGATGGGACAGATCTGGCGAGCTGGCG 339
OY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 340 CCCCTGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
OY 81 PheProGlyMetGlySerGlnGlnLeuArgLeuAlaSerPheTyraPstProLeuThr 100
Db 400 TTCCCGGACATGGGCTGTGAGAGATGGGCTGTGGCTCTCTTAAGACTGGCGCTGACT 459
OY 101 AlaGlnValProProGlnLeuLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 460 GCTGAGGTGCACCCGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 519
OY 121 LysValAlaArgCysPhePheCysTyrglyLeuGlnSerTrpLysArgGlyAspAspPro 140
Db 520 AAGGTGAGTGTCTTCTGTGATGGGGGCTGCAGAGCTGGAGCGGGGAGAGAGAGAG 579
OY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerIstRpArg 160
Db 580 TGGACGGAGCATGCCAAGTGGTCCCGCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 639
OY 161 AspPheValHisSerValGlnGlnLysHisSerGlnLeuLeuGlnGlnGlnGlnGlnGln 180
Db 640 GACTTTGTCCACAGTGTGCAGAGACTCACTCCAGCTGTGGGCTCTGGAGACCCGTGG 699
OY 181 GlnGlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyraProGln 200
Db 700 GAAGAACCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
OY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnProGlyValaArgAsp 220
```

Db 760 CTGCCACACCCAGAGAGAGTCCAGTCTGAAAGTCCAGAGCCAGAGCCAGGAT 819
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysLysValCysLeuAspArg 240
Db 820 GTGGAGGGCGGAGCTCGGCGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
Db 880 GCCGTCTCATGCTTTTGTGCGTGGCCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 940 CTGCAGCTGTGCCCATCTGCAGAGAGCCCGCTCCGAGCCCGCGAGCCGACCTTCTGTCC 999

RESULT 4
PCT-US03-20821-4
Sequence 4, Application PC/TUS0320821
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
FILE REFERENCE: ISIS0037-500
CURRENT APPLICATION NUMBER: PCT/US03/20821
PRIOR FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 10/188,646
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 4
LENGTH: 1260
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (174)...(1016)
PCT-US03-20821-4

Alignment Scores:
Pred. No.: 4,266-266 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
Gaps: 0

US-09-762-577b-12 (1-309) x PCT-US03-20821-4 (1-1260)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 174 ATGGAGCTTAAGACAGTGCAGAGTGCCTGCACCGTGGACCAAGCCGAGCCAGCTGGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValIleu 40
Db 234 GCGGTGATGTGTCCACGAGAGAGCGCTGTGAGCCCGCTCTCTGGAGAGCCCTTCTCTA 293
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 294 GGCCTGGACCTCGAGAGCTGGAGCAAGTGGACAGTGGATGGCAGATCTTGGCCAGCTGGG 353
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCTGACAG 413
QY 81 PheProGlyMetGlySerGlnGlnLeuValAspPheTyrAspTrpProLeuThr 100
Db 414 TTCCTGGAGTGGCTCTGAGAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 473
QY 101 AlaGluValProProGlyLeuLeuValAlaAlaGlyPhePheHisTrpGlyHisGlnAsp 120
Db 474 GCTGAGGTGCAACCCGAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 533
QY 121 LysValArgCysPhePheCysTyrGlyGlnGlnSerTrpLysArgLysAspAspPro 140

Db 534 AAGGTAGGTGCTTCTTCTGCTATGAGGGGCTTCGACAGACTGGAAAGCCGGGAGACAGACCC 593
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 594 TGACGGAGACATCCAGAGTGTTCCTCCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 653
QY 161 AspPheValHisSerValGlnGlnHisSerGlnLeuGlnGlnGlnGlnGlnGlnGlnGln 180
Db 654 GACTTGTTCACAGTGTGCTGAGAGAGACTCACTCCAGCTGTGCTGTGCTGTGCTGTGCTGTG 713
QY 181 GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 714 GAAGAAGCCGGAAG 773
QY 201 LeuProTrpProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220
Db 774 CTGCCACACCCAGAGAGAGAGTCCAGTGAAGTCCCGCAGAGCCAGAGCCAGGAGAT 833
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 893
Db 834 GTGGAGCGGAGCTGGCGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGly 260
Db 894 GCGGTCTCATGCTTTTGTGCGTGGCCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGCAGCTGTGCCCATCTGCAGAGAGCCCGCTCCGAGCCCGCGAGCCGACCTTCTGTCC 1013

RESULT 5
US-10-170-235-27143
Sequence 27143, Application US/10170235
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
FILE REFERENCE: C1001380
CURRENT APPLICATION NUMBER: US/10/170,235
PRIOR FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 27143
LENGTH: 1260
TYPE: DNA
ORGANISM: HUMAN
US-10-170-235-27143

Alignment Scores:
Pred. No.: 4,266-266 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
Gaps: 0

US-09-762-577b-12 (1-309) x US-10-170-235-27143 (1-1260)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db 174 ATGGAGCTTAAGACAGTGCAGAGTGCCTGCACCGTGGACCAAGCCGAGCCAGCTGGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
Db 234 GCGGTGATGTGTCCACGAGAGAGCGCTGTGAGCCCGCTCTCTGGAGAGCCCTTCTCTA 293
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 294 GGCCTGGACCTCGAGAGCTGGAGCAAGTGGACAGTGGATGGCAGATCTTGGCCAGCTGGG 353
QY 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCTGACAG 413

Qy 81 PheProglYMeTgLYSeRgluGluLeuAArgLeuAlaSerPheTYrAspTrpProLeuThr 100
Db 414 TTCCCGGCGATGGGCTCTGAGAGTTGGCTCTGGCTCTCTTATGACTGGCGCTGACT 473
Qy 101 AlaGluValProProgluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGGCCACCGAGCTGCTGGCTGGCTGGCTCTTTCACACAGGCGCATCAGAGC 533
Qy 121 LysValAlaArgCySPhePheCySTyrgLYglYLeuGlnSerTrpLYsArgGlyAspAspPro 140
Db 534 AAGGTGAGGTGGCTTCTTCTGCTATGGGGCCCTGCGAGCTGGAAACGGGGGACACACCC 593
Qy 141 TrpThrGlnHisAlaLYsTrpPheProSerCySGlnPheLeuLeuArgSerLYsGlyArg 160
Db 554 TGGACGAGCATGCCAAGTGGTTCCCGAGCTGTCACTTCTGCTCGGTCAAAAGGAAGA 653
Qy 161 AspPheValHisSerValGlnGlnuThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db 654 GACTTGTCCACAGTGTGCGAGGAGACTCACTCCGAGCTGGTGGGCTCTTGGGACCCGTGG 713
Qy 181 GluGluProgluAspAlaAlaProValAlaProSerValProAlaSerGlyTYrProglu 200
Db 714 GAAGAACCGGAGAGAGCAGCCCTGTGGCCCTCTCCCTGCTGGGTGACCTGAG 773
Qy 201 LeuProThrProArgArgGluValGlnSerGlnuSerAlaGlnuProgluValAlaArgAsp 220
Db 774 CTGCCACACCCAGAGAGAGGTCCAGTCTGAAAGTGCACAGAGCCAGAGCCAGAGGAT 833
Qy 221 ValGluAlaGlnLeuArgArgLeuGlnGlnuArgThrCySbLYsValCYsLeuAspArg 240
Db 834 GTGGAGGGCAGCTGCGCGCGCTGCGAGAGAGAGAGAGTGTGCTGGACCGC 893
Qy 241 AlaValSerLYsLeuValPheValProCySGlyHisLeuValCYsAlaGlyCYsAlaProGly 260
Db 894 GCCGTGTCCATGCTCTTGTGTGCGCGCCGACCACTGTGTGTGAGTGTGCCCGCGC 953
Qy 261 LeuGlnLeuCySProLYsCySPheArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGCAGCTGTGCCCATCTGCAGAGACCCCGTCCGACCGCGTGGCAGCTTCTGTGCC 1013

RESULT 6
US-10-188-646-4
; Sequence 4, Application US/10188646
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennet
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 4
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1016)
US-10-188-646-4

Alignment Scores:
Pred. No.: 4.26e-266 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 42 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-188-646-4 (1-1260)
Qy 1 MetGlyProLYsAspSerAlaLYsCySLeuHisArgGlyProGlnProSerHisTrpAla 20

Db 174 ATGGGACCTTAAGACAGTCCCAAGTGCCTGTGACCCGTGGACCAACAGCCGACCTGGGCA 233
Qy 21 AlaGlyAspGlyProThrGlnGluArgCYsGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGTGATGTGCTCCACGACAGAGCGCTGTGACCCCGCTCTGTGGAGCCCTGTCTCTTA 293
Qy 41 GlyLeuAspThrCYsArgAlaTrpAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 294 GGCTGTGACACCTTCACAGCCCTGGAGCACCGTGTATGGGAGATCTGGGGCAGACTGGC 353
Qy 61 ProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 354 CCCCTGACAG 413
Qy 81 PheProglYMeTgLYSeRgluGluLeuAArgLeuAlaSerPheTYrAspTrpProLeuThr 100
Db 414 TTCCCGGCGATGGGCTCTGAGAGATTGCTGTGCTCTCTTCTATGACTGGCGCTGACT 473
Qy 101 AlaGluValProProgluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGGCCACCGAGCTGCTGGCTGGCTGGCTCTTCTTCCACACAGGCGCATCAGAGC 533
Qy 121 LysValAlaArgCySPhePheCySTyrgLYglYLeuGlnSerTrpLYsArgGlyAspAspPro 140
Db 534 AAGGTGAGGTGGCTTCTTCTGCTATGGGGCCCTGCGAGCTGGAAACGGGGGACACACCC 593
Qy 141 TrpThrGlnHisAlaLYsTrpPheProSerCySGlnPheLeuLeuArgSerLYsGlyArg 160
Db 594 TGGACGAGCATGCGCAAGTGGTTCCCGAGCTGTCACTTCTGCTCGGTCAAAAGGAAGA 653
Qy 161 AspPheValHisSerValGlnGlnuThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
Db 654 GACTTGTCCACAGTGTGCGAGGAGACTCACTCCGAGCTGGGCTCTTGGGACCCCGTGG 713
Qy 181 GluGluProgluAspAlaAlaProValAlaProSerValProAlaSerGlyTYrProglu 200
Db 714 GAAGAACCGGAGAGAGAGCCCTGTGGCCCTCTCCCTGCTGGGTGACCTGAG 773
Qy 201 LeuProThrProArgArgGluValGlnSerGlnuSerAlaGlnuProgluValAlaArgAsp 220
Db 774 CTGCCACACCCAGAGAGAGGTCCAGTCTGAAAGTGCACAGAGCCAGAGCCAGAGGAT 833
Qy 221 ValGluAlaGlnLeuArgArgLeuGlnGlnuArgThrCySbLYsValCYsLeuAspArg 240
Db 834 GTGGAGGGCAGCTGCGCGCGCTGCGAGAGAGAGAGAGTGTGCTGGACCGC 893
Qy 241 AlaValSerLYsLeuValPheValProCySGlyHisLeuValCYsAlaGlyCYsAlaProGly 260
Db 894 GCCGTGTCCATGCTCTTGTGTGCGCGCCGACCACTGTGTGTGAGTGTGCCCGCGC 953
Qy 261 LeuGlnLeuCySProLYsCySPheArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 954 CTGCAGCTGTGCCCATCTGCAGAGACCCCGTCCGACCGCGTGGCAGCTTCTGTGCC 1013

RESULT 7
US-10-553-355-11
; Sequence 11, Application US/10553355
; GENERAL INFORMATION:
; APPLICANT: Deutsches Krebsforschungszentrum
; TITLE OF INVENTION: Livin-specific siRNAs for the treatment of therapy-resistant tumors
; FILE REFERENCE: DK62169PC
; CURRENT APPLICATION NUMBER: US/10/553,355
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: EP 0300 8081.6
; PRIOR FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-553-355-11

Alignment Scores:

Pred. No.: 4,266-266 Length: 1260
 Score: 280.00 Matches: 280
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 90.6% Indels: 0
 DB: 52 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-553-355-11 (1-1260)

```

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrPala 20
Db 174 ATGGACCTTAAGACAGTGCACAGTGCCTGACCGTGGACCAACAGCCGACCTGGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGTGATGGTCCACGACGAGAGCGCTGTGGACCCGCTCTCTGGGCAACCTGTCTTA 293
QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 294 GGCTTGGACACTGTCACAGAGCTGGGACCACTGGATGGAGATCTTGGGCAAGTGGCG 353
QY 61 ProLeuThrGlnGluGlnGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
Db 354 CCCCTGACAGAGGAGAGAGAGAGAGGCGCGGGGCCACTTGTCCAGGGGGCTGCC 413
QY 81 PheProGlyMetGlySerGlnGluGluArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db 414 TTCCCGGCAATGGGCTTGAAGAGTTCGCTGAGCTCTTCTATACATGGCCGCTGACT 473
QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGCACCCGAGCTGCTGGCTGCTGCCGGCTTCTCCACAGGCCATCCAGAC 533
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
Db 534 AAGGTGAGGTCTTCTCTGCTATGGGGCTTCAAGCTCGAAGCGCGGAGCAGACCCC 593
QY 141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 594 TGGACGAGCATGCACAAAGTGTCTCCAGCTGTCACTTCTGCTCCGGTCAAAAGAGAGA 653
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 654 GACTTGTCTCCACAGTGTGCAGAGACTCTCCAGCTGCTGGGCTCTGGGACCCGTGG 713
QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
Db 714 GAAGAACCGGAACACCCAGCCCTGTGGCCCTCTCCGTCTGTGGTAACTCTGAG 773
QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGluProGlyValaArgAsp 220
Db 774 CTGCCACACCCGAGAGAGGTCCAGTCTGAAGTGCACAGAACCCAGAACCCGAGAT 833
QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCysLeuAspArg 240
Db 834 GTGGAGCCGCAAGCTGGCGGCTGCAGAGAGAGAGACGTCGCAAGGTGTGCTGAGCCG 893
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
Db 894 GCGGTCTCCATCGTCTTGTGTGCGGTGGCCACCTGTGTCTGAGTGTGCCCCCGGC 953
QY 261 LeuGlnLeuCysProIleCysArgAlaProValaArgSerArgValaArgThrPheLeuSer 280
Db 954 CTGCAGCTGTGCCCATCTGCAGAGCCCGCTCCGACCCGGGTGCGACCTTCTGTCC 1013

```

RESULT 8

US-10-940-774-1949
 ; Sequence 1949, Application US/10940774
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/10/940,774
 ; CURRENT FILING DATE: 2004-09-15
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1949
 ; LENGTH: 1260
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-940-774-1949

Alignment Scores:

Pred. No.: 4,266-266 Length: 1260
 Score: 280.00 Matches: 280
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 90.6% Indels: 0
 DB: 63 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-940-774-1949 (1-1260)

```

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrPala 20
Db 174 ATGGACCTTAAGACAGTGCACAGTGCCTGACCGTGGACCAACAGCCGACCTGGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGTGATGGTCCACGACGAGAGCGCTGTGGACCCGCTCTCTGGGCAACCTGTCTTA 293
QY 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnLeuGlyGlnLeuArg 60
Db 294 GGCTTGGACACTGTCACAGAGCTGGGACCACTGGATGGAGATCTTGGGCAAGTGGCG 353
QY 61 ProLeuThrGlnGluGlnGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
Db 354 CCCCTGACAGAGGAGAGAGAGAGGCGCGGGGCCACTTGTCCAGGGGGCTGCC 413
QY 81 PheProGlyMetGlySerGlnGluGluArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db 414 TTCCCGGCAATGGGCTTGAAGAGTTCGCTGAGCTCTTCTATACATGGCCGCTGACT 473
QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGCACCCGAGCTGCTGGCTGCTGCCGGCTTCTCCACAGGCCATCCAGAC 533
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
Db 534 AAGGTGAGGTCTTCTCTGCTATGGGGCTTCAAGCTCGAAGCGCGGAGCAGACCCC 593
QY 141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 594 TGGACGAGCATGCACAAAGTGTCTCCAGCTGTCACTTCTGCTCCGGTCAAAAGAGAGA 653
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 654 GACTTGTCTCCACAGTGTGCAGAGACTCTCCAGCTGCTGGGCTCTTGGGACCCGTGG 713
QY 181 GlnGluProGluAspAlaAlaProValaAlaProSerValProAlaSerGlyTyrProGlu 200
Db 714 GAAGAACCGGAACACCCAGCCCTGTGGCCCTCTCCGTCTGTGGTAACTCTGAG 773
QY 201 LeuProThrProArgArgGlnValGlnSerGlnSerAlaGlnGluProGlyValaArgAsp 220
Db 774 CTGCCACACCCGAGAGAGGTCCAGTCTGAAGTGTGCCAGAGCCAGAGCCGAGAT 833
QY 221 ValGlnAlaGlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCysLeuAspArg 240

```

```

Db      834 GTGGAGGCGCCAGCTGGCGGGCGTGCAGAGAGAGAGACGTCGCAAGTGTGCTCGACCCG 893
Oy      241 AlaValSerIleValAlaPheValProCysGlyIshLeuValCysAlaGluCysAlaProGly 260
Db      894 GCCGTGTCATCTGCTTTGTGTGCCGGCCGACCTGCTGTGCTAGTGTGCCCCGGC 953
Oy      261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValaIArgThrPheLeuSer 280
Db      954 CTGCAGCGTGTGCCCATCTCGACAGAGCCCGCCGTCGAGCGCGCTGCGCACCTTCTGTCC 1013

RESULT 9
US-10-940-774A-1949
: Sequence 1949, Application US/10940774A
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307
: CURRENT APPLICATION NUMBER: US/10/940,774A
: PRIOR FILING DATE: 2004-09-15
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1949
: LENGTH: 1260
: TYPE: DNA
: ORGANISM: Human
US-10-940-774A-1949

```

Alignment Scores:		
Pred. No.:	4,266-266	Length: 1260
Score:	280.00	Matches: 280
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	90.6%	Indels: 0
DB:	64	Gaps: 0

QY	1	MeGlyIProLysAspSerLalysCysLeuHiIsaTgGIYPProGInProSerHisITPAla	20
Db	174	ATGGAGACCTAAAGACAGTCCCAAGTCCCTGCACCCGTGACACAGCCAGCCACTGGGCA	233
QY	21	AlaGlyAspGlyProThrGInGInGluArgCysGlyProArgSerLeuGlySerProValLeu	40
Db	234	GCCGGTGAATGTCCTCCACGAGAGGCGCTGTGAACCCCGCTCTGTGGGAGCCCTGTCTTA	293
QY	41	GlyLeuAspThrCysArgLalATrAspHisValAspGlyGInIleLeuGlyGInLeuArg	60
Db	294	GGCCTTGACACTCTGCAGAGCTTGGACACAGTGAATGGACAGATCTCGGCGACCTCGG	353
QY	61	ProLeuThrGInGInGInGInGInGInGInGInGInGInGInGInGInGInGInGInGIn	80
Db	354	CCCTTACAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	413
QY	81	PheProGlyMeGlySerGInGInGInGInGInGInGInGInGInGInGInGInGInGInGIn	100
Db	414	TTCCCGGCAATGGGCTCTAGAGATTTGGCTCTGGCGCTCTTCTATGACTGGCCGCTACT	473
QY	101	AlaGlyValProProGInLeuLeuLalalalaglyPhePheHisIsthGlyHisGInAsp	120
Db	474	GCTGAGGTGCAACCCGAGCTGCTGGGTGTGCGGCTCTTCCACACAGGCGCATCAGAC	533
QY	121	LysValAlaGlySerPhePheCysTyrGlyGlyLeuGInSerITrLysArgGlyAspAspPro	140
Db	534	AAGGTAGGAGCTTTCTTCTGCTATGGGGGCTGCAGACCTGGAAAGCGGGGAGACACCC	593
QY	141	TrpThrGInHisAlaLysITrPheProSerCysGInPheLeuLeuAspSerLysGlyArg	160

Db	594	TTGAGCGGAGCATGCCAAGTGGTCTCCCAAGCTGTGAGTTCCCTCCGATCAAAAGGA	653
Qy	161	AspPheValHisSerValGlnGluIleThrHisSerGlnLeuLeuGlySerTrpAspProThr	180
Db	654	GACCTTGTCCACAGTGTGCAGAGACTACTCCAGCTGCTGGGCTCTTGGGACCCGTGG	713
Qy	181	GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu	200
Db	714	GAAAGAACGGAAAGCAGACCCCTGTGGCCCCCTCCGTCCTGGCTCTGGGATACCTTAG	773
Qy	201	LeuProThrProAlaGArgGluValGlnSerGlnSerAlaGlnGluProGlyValaArgAsp	220
Db	774	CTGCCACACACCAGAGAGAGAGTCCAGCTGAAGTGCCCGCAGAGACCAGACGAGAT	833
Qy	221	ValGluAlaGlnLeuAlaArgArgLeuGlnGlnGlnIleuArgThrCysIleValCysLeuAspArg	240
Db	834	GTTGAGGGGCGAGCTGCCGGCGCTCCAGAGAGAGAGAGCTGCCAAGGTGTGCTCTGACCGC	893
Qy	241	AlaValSerIleValAlaPheValProCysGlyHisIleuValCysAlaGluCysAlaProGly	260
Db	894	GCCGGTCCATCGTCTTGTGTCCCGTGGCGGCCACCTGGTGTGTGCTGATGTGGCCCCCGGC	953
Qy	261	LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer	280
Db	954	CTGCAGCTGTGCCCCCATCTGCAGAGACCCCGCGTCCGACACCGCGTGCACCTTCTCTGTCC	1013

```

RESULT 10
PCT-US02-29560-182
; Sequence 182, Application PC/TUS0229560
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Heyezl, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560
; CURRENT FILING DATE: 2025-11-01
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 1268
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-29560-182

```

Pred. No.:	4,286-266	Length:	1268
Score:	280.00	Matches:	280
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	90.6%	Indels:	0
DB:	1	Gaps:	0
US-09-762-577B-12 (1-309) x PCT-US02-29560-182 (1-1268)			
QY	1	MeG1PProlysaPseSer1alalysCysLeuH1a1rG1yProGlnProSeH1e1rYp1a	20
Db	174	ATGGGACCTPAAGACAGACGTGCCAAGTCCCTGCACCGTGAACCAAGCGAGCACTGGGCA	233
QY	21	AlAG1yAspG1yProthrGlnGlnLarGysG1yProAlgSerLeuG1ySerProValLeu	40
Db	234	GCCGGGAAAGTGTCCACGCAAGGAGCGCTGTGAACCCCTCTCTGGGAGGCCCTGTCTTA	293
QY	41	G1yLeuAspThrCysa1rGln1a1rPasp1aVala1rG1yGln1e1rG1yGlnLeuArg	60


```

; APPLICANT: Reisfeld, Ralph A.
; TITLE OF INVENTION: The Scripps Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE REFERENCE: TSRI-874.1PC
; CURRENT APPLICATION NUMBER: PCT/US04/08932
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: 60/457,009
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1268
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(1016)
PCT-US04-08932-28

Alignment Scores:
Pred. No.: 4,286-266 Length: 1268
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 3 Gaps: 0

US-09-762-577B-12 (1-309) x PCT-US04-08932-28 (1-1268)
QY 1 MetGlyProLyAspSerAlaLysCyLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 174 ATGGAGCTTAAGACAGTGCACAGTGCCTGCACCGTGAGCCAGCCAGCCACTGGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 234 GCCGGTATGTCTCCACCGCAGAGAGCGCTGTGGACCCCGCTCTCTGGGAGCCCTGTCTTA 293
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyLeuArg 60
DB 294 GGCTGGACACCTGCAGAGCCTGGGACCACTGATGGAGGACATCTGGGCGCAGCTGGCG 353
QY 61 ProLeuThrGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
DB 354 CCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY 81 PheProGlyMetGlySerGlyLeuArgLeuLeuAspSerPheTyrAspTrpProLeuThr 100
DB 414 TTCCCGGCGATGGGCTCTGAGAGAGTGGCTGTGGCTCTCTTATGACTGGCCGCTGACT 473
QY 101 AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisTrpGlyHisGlnAsp 120
DB 474 GCTGAGGAGCCAGCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpPheArgGlyAspAspPro 140
DB 534 AAGGTGAGAGTCTTCTCTCTATGAGGAGCTGAGAGCTGAGAGCGGAGGAGAGAGCC 593
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLeuGlyArg 160
DB 594 TGGAGCGAGCATGCTCCAGAGTGTCTCCAGCTGTCACTTCTGCTCTGGTCAAAAGAGAA 653
QY 161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 654 GACTTTGTCACAGTGTGTCAGAGAGCTCCTCCAGCTGCTGGGCTCTGGGAGCCCGTGG 713
QY 181 GlnGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu 200
DB 714 GAAGAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773
QY 201 LeuProThrProArgArgGluValGlnSerGlyLeuSerAlaGlnGluProGlyValArgAsp 220
DB 774 CTGCCACACCCAGAGAGAGAGAGTCCAGTCTGAAGTGTGCCAGAGAGCCAGAGAGGAT 833
```

```

QY 221 ValGluAlaGlnLeuArgArgLeuGlnGluArgThrCysIysValCysLeuAspArg 240
DB 834 GTGAGAGCGCAGAGCTGCGCGGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY 241 AlaValSerLeuValPheValProCysGlyHisIleValCysAlaGluCysAlaProGly 260
DB 894 GCCGTGTCAATCGCTTTGTGTGCGGTGGCCACCTGTGTGTGAGTGTGCCCCGCG 953
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 954 CTGAGCTGTGCCCCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013

RESULT 13
US-10-245-882-182
; Sequence 182, Application US/10245882
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-002710US
; CURRENT APPLICATION NUMBER: US/10/245,882
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/323,887
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/325,114
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/340,944
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/355,145
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/355,257
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/369,899
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/372,246
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 1268
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-245-882-182

Alignment Scores:
Pred. No.: 4,286-266 Length: 1268
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 43 Gaps: 0

US-09-762-577B-12 (1-309) x US-10-245-882-182 (1-1268)
QY 1 MetGlyProLyAspSerAlaLysCyLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 174 ATGGAGCTTAAGACAGTGCACAGTGCCTGCACCGTGAGCCAGCCAGCCACTGGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 234 GCCGGTATGTCTCCACCGCAGAGAGCGCTGTGGACCCCGCTCTCTGGGAGCCCTGTCTTA 293
```


[illegible]

```

RESULT 14
US-10-807-897-28
; Sequence 28, Application US/10807897
; GENERAL INFORMATION:
; APPLICANT: Xiang, Rong
; APPLICANT: Zhou, He
; APPLICANT: Reisfeld, Ralph A.
; TITLE OF INVENTION: The Scripps Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE REFERENCE: TSRI-874.1
; CURRENT APPLICATION NUMBER: US/10/807,897
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,009
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1268
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174) ... (1016)

```

US-10-807-897-28	
Alignment Scores:	
Pred. No.:	4,28e-266
Score:	280.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	90.6%
DB:	62
Length: 1268	
Matches:	280
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-762-577B-12 (1-309) X US-10-807-897-28 (1-1268)

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20

Db 174 ATGGGACCTTAAGACAGATGCGCAAGTGCCTGCACCGTGACCAAGCCGACCTGGGCA 233

Dy 21 A l a g i y a s p g i y p r o t h r g i n g l u n r g c y s e g l y p r o a r g s e r l e u c i y s e r p r o v a l e u 40
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 234 G C C G S T G A R G S T C C C A C G C A G A G C G C T G T G A C C C C G C T C T C T G G C A G C C C T G T C C T A 293

Qy 41 GlyLeuAspThrCysArgAlaTyrAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 294 GGCTTGACACCTGAGAGCTGGACCACTGGATGGGCAATCTCTGGGCCAGCTGGG 333

Dy 61 ProLeuThrGluGluGluGluGluGluAlaIleThrLeuSerArgGlyProAla 80
| | | | | | | | | | | | | | | | | | | | | |
Db 354 CCCCTGCAGAGAGGAAGAAGAGAGAGCGCCGGGGGCCACCTTGTTCAGGGGGCCTTGC 413

QY 81 PhneDroGIyMeGtYserGIuGlueuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
|||
Db 414 TTCCCGGATGGGCTCTGTAGGAGTGGCGCTGTGGCTCCCTTTATAGTCTGGCGGCTAGCT 473

Dy 101 AlaGluValProProGluLeuLeualaalaaglyphepheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTCCACCCGAGCTGCTGGCTGCTGCCGCTTCTTCACACAGGCCATCAGAAC 533

QY 121 LysValaIaGcysPhePheCysTyrGlyGlyLeuGlnserTrpLysArgGlyAspAspPro 140
Dp 534 AAGGTGAAGCTGCTTCTTCTGCTAAGGGGGGCTGAGAGCTGGAAGCGCGGGGACGACCCC 593

QY 141 TPTHTGIIHIIAIALYSTTPHPHROSERCYSGINPHEULEUARGSERLYSGIARG 160
Dp 594 TGGACGGAGCATGCCAAGTGTCCCAAGTGTGTCTCTGTCGGGTCAAAAGGAGA 653

QY 161 AAPPheValHisSerValGlnGluThrHisSerGlnLeuGlySerTrpAspProTyr 180
|||
Dp 654 GACTTGTGCCACAGTGTGCAGGAGACTACTCCAGCTGTGGCTCTTGGGACCCGTGG 713

DY 181 GIUGIUPROGLUASPAAIAAPROVALAIPROSERVAIPROALASERGIYYTYPROGU 200
| | | | | | | | | | | | | | | | | | | | |
DB 714 GAAGAACCGGAAGACGACCCTGTGGCCCCCCTCCGTCCTTG6TTACCTTAG 773

QY 201 LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGlyAlaArgAsp 220
Dd 774 CTGCCACACCCAGAGAGAGGTCCAGTCTGAAGTCCCGACGACCGACCGGAT 833

QY 221 ValGlnValGlnLeuArgArgIleGlnIleGlnIleArgThrCysIysValCysLeuAspArg 240
|||
D8 834 GCGAGCGCGCAGCTGCGCGCGCGCTGCAGAGAGAGAGGAGCCTGCAGAGCTGTCTCTGAGCCGC 893

DQ 241 AAlaValSerIleValPheValProCysGlyHisIleValCysAsnGluCysAlaProGly 260
Dd 894 GCCGTGCATCGTCTTTGTGCCGTGGCCACCTGATTGTGTGAAGTGCCCCGGC 953

Qy	261	LeuGluLeuCySProlleCySaArgAlaProValArgSerArgValArgThrPheLeuSer	280
Db	954	CTGCACTGTGCCCCATCTGCAGAGCCCCCGTCGCGACGCCGCGTGGCACTTCTCTGTCC	1011

RESULT 15
US-60-685-372-1181
: Sequence 1181, Application US/60685372

APPLICANT: Belouchi, Abdelmajid

APPLICANT: Raelson, John V
APPLICANT: Bradley, Walter E
APPLICANT: Paguin, Bruno
APPLICANT: Nguyen-Huu, Quynh
APPLICANT: Croteau, Pascal
APPLICANT: Allard, Rene
APPLICANT: Little, Randall D
APPLICANT: Cousineau, Johanne
APPLICANT: Berdewegh, Paul V
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
FILE REFERENCE: 059908-5005-PR
CURRENT APPLICATION NUMBER: US/60/685,372
CURRENT FILING DATE: 2005-05-31
NUMBER OF SEQ ID NOS: 2738
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1181
LENGTH: 1268
TYPE: DNA
ORGANISM: Homo sapiens
US-60-685-372-1181

Alignment Scores:
Pred. No.: 4,286-266 Length: 1268
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 82 Gaps: 0

US-09-762-577B-12 (1-309) x US-60-685-372-1181 (1-1268)

QY 1 MetGlyProLyAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
DB 174 ATGGGACCTAAAGACAGTGCCTGACCTGGACACAGCCAGCCACATCGGACA 233
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
DB 234 GCCGGTGAATGCTCCACCGAGAGCGCTGTGACCCCGCTCTCTGGGACGCCCTGTCTTA 293
QY 41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
DB 294 GGCCCTGGACACCTGGAGAGCCTGGGACCACTGGATGGCAGATCTGGCCACGCTGGCG 353
QY 61 ProLeuThrGlnGluGlnGluGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 354 CCCCTGACAG 413
QY 81 PheProGlyMetGlySerGlyGlnLeuArgLeuAlaSerPheTrpAspTrpProLeuThr 100
DB 414 TTCCCGGCGATGGCTGTGAGGAGTGGCTGTGGCTCTTCTATGACTGGCCGCTGACT 473
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
DB 474 GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533
QY 121 LysValArgCysPhePheCysTrpGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
DB 534 AAGGTGAGGTCTTCTTCTGCTATGGGGCTGTCAGAGCTGGAAGCGGGGAGCAGACCC 593
QY 141 TrpThrGlnHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
DB 594 TGGACGAGCATGCGCAAGTGTTCCTCCAGCTGTCAATCTGCTGCTGCTGCTGCTGCTGCT 653
QY 161 AspPheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
DB 654 GACTTTGTCCACAGTGTGACAGAGACTCATCTCCAGCTGCTGGGCTCTGGGACCCGCTG 713
QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTrpProGlu 200
DB 714 GAAGAACCGAG 773
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGlnProGlyAlaArgAsp 220

DB 774 CTGCCACACCCAGAGAGAGAGTCTGAAGTGCCTCAGAGCCAGAGCCAGAGGAT 833
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
DB 834 GTGAGGCGGACGCTGCGCGGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893
QY 241 AlaValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGly 260
DB 894 GCCGTGTCCATCGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
DB 954 CTGACGCTGTGCTCCATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013

Search completed: April 24, 2006, 11:51:02
Job time : 6656 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2006, 10:00:00 ; Search time 2335 Seconds

(without alignments)
429.649 Million cell updates/sec

Title: US-09-762-577B-12

Perfect score: 309
Sequence: 1 MGPRDSAKCLHRGPQPSHWA.....GLQGLPAPLCLFWTFWMAC 309

Scoring tables:

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 7548307 seqs, 1623350438 residues

Word sizes: 1

Total number of hits satisfying chosen parameters: 15092329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-O=/abse/ABSSWEB_spool/US09762577/runat_24042006.105934.1148/app_query.fasta_1
-DB=Pending Patents NA New -OFTM=fastcat -SUFFIX=p2nol1.tmpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -IDITS=bits -STAR=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs03p
-USER=US09762577 @CGN 1 1 803 @runat_24042006.105934.1148 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Pending Patents NA New.*

1: /SIDS5/ptodata/2/pna/PCT_NEW_COMB.seq.*
2: /SIDS5/ptodata/2/pna/US05_NEW_COMB.seq.*
3: /SIDS5/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /SIDS5/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /SIDS5/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq.*
8: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq.*
9: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq.current.*
10: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq1.*
11: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq2.*
12: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq3.*
13: /SIDS5/ptodata/2/pna/US60_NEW_COMB.seq.*
14: /SIDS5/ptodata/2/pna/US60_NEW_COMB.seq.current.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280	90.6	1246	5	US-09-762-577B-11
2	280	90.6	1260	11	US-11-266-748A-23550
3	248	80.3	1000	11	US-11-266-748A-290500

C	4	248	80.3	1000	11	US-11-266-748A-341929	Sequence 341929, A
C	5	119	38.5	633	11	US-11-266-748A-211754	Sequence 211754, A
C	6	119	38.5	633	11	US-11-266-748A-235360	Sequence 235360, A
C	7	18	5.8	226	5	US-09-762-577B-49	Sequence 49, Appl
C	8	14	4.5	634	11	US-11-266-748A-41998	Sequence 41998, A
C	9	14	4.5	927	11	US-11-266-748A-15520	Sequence 15520, A
C	10	14	4.5	927	11	US-11-266-748A-21170	Sequence 21170, A
C	11	14	4.5	934	11	US-11-266-748A-13769	Sequence 13769, A
C	12	14	4.5	1000	11	US-11-266-748A-115538	Sequence 115538, A
C	13	14	4.5	1000	11	US-11-266-748A-157702	Sequence 157702, A
C	14	14	4.5	1000	11	US-11-266-748A-220957	Sequence 220957, A
C	15	14	4.5	1000	11	US-11-266-748A-224572	Sequence 224572, A
C	16	14	4.5	1000	11	US-11-266-748A-284932	Sequence 284932, A
C	17	14	4.5	1000	11	US-11-266-748A-293814	Sequence 293814, A
C	18	14	4.5	1000	11	US-11-266-748A-336361	Sequence 336361, A
C	19	14	4.5	1000	11	US-11-266-748A-345243	Sequence 345243, A
C	20	14	4.5	1000	11	US-11-266-748A-395081	Sequence 395081, A
C	21	14	4.5	1000	11	US-11-266-748A-395082	Sequence 395082, A
C	22	14	4.5	1000	11	US-11-266-748A-405947	Sequence 405947, A
C	23	14	4.5	1000	11	US-11-266-748A-466127	Sequence 466127, A
C	24	14	4.5	1000	11	US-11-266-748A-466128	Sequence 466128, A
C	25	14	4.5	1000	11	US-11-266-748A-476993	Sequence 476993, A
C	26	14	4.5	1108	11	US-11-266-748A-262721	Sequence 262721, A
C	27	14	4.5	1108	11	US-11-266-748A-323238	Sequence 323238, A
C	28	14	4.5	1115	11	US-11-266-748A-69151	Sequence 69151, A
C	29	14	4.5	1115	11	US-11-266-748A-121962	Sequence 121962, A
C	30	14	4.5	1746	11	US-11-266-748A-186758	Sequence 186758, A
C	31	14	4.5	2416	9	US-11-334-902-41	Sequence 41, Appl
C	32	14	4.5	2416	11	US-11-316-539-41	Sequence 41, Appl
C	33	14	4.5	2580	9	US-11-334-902-7	Sequence 7, Appl
C	34	14	4.5	2580	11	US-11-316-539-7	Sequence 7, Appl
C	35	14	4.5	3076	11	US-11-266-748A-59049	Sequence 59049, A
C	36	14	4.5	3496	7	US-10-567-667-1281	Sequence 1281, Ap
C	37	14	4.5	5243	1	PCT-US06-05584-726	Sequence 726, Ap
C	38	11	3.6	1344	11	US-11-266-748A-80530	Sequence 80530, A
C	39	11	3.2	1344	11	US-11-266-748A-133341	Sequence 133341, A
C	40	10	3.2	266	9	US-11-331-019-43184	Sequence 43184, A
C	41	10	3.2	555	11	US-11-266-748A-45314	Sequence 45314, A
C	42	10	3.2	555	11	US-11-266-748A-212950	Sequence 212950, A
C	43	10	3.2	2086	11	US-11-266-748A-26831	Sequence 26831, A
C	44	10	3.2	2540	6	US-10-533-519-1159	Sequence 1159, Ap
C	45	10	3.2	2540	9	US-11-334-902-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-762-577B-11
Sequence 11, Application US/09762577B
GENERAL INFORMATION:
APPLICANT: Dranoff, Glenn
APPLICANT: Schmoltinger, Jan
APPLICANT: Hodi, F. Stephen
APPLICANT: Mollick, Joseph
TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
FILE REFERENCE: 2486/109
CURRENT APPLICATION NUMBER: US/09/762,577B
PRIORITY FILING DATE: 2002-08-29
PRIORITY FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1246
TYPE: DNA
ORGANISM: homo sapiens
US-09-762-577B-11

Alignment Scores:
Pred. No.: 5.35e-267
Score: 280.00
Percent Similarity: 100.0%
Best local Similarity: 100.0%
Length: 1246
Matches: 280
Conservative: 0
Mismatches: 0

Query Match: 90.6% Indels: 0
DB: 5 Gaps: 0

US-09-762-577b-12 (1-309) x US-09-762-577b-11 (1-1246)

```

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db 160 ATGGGACCTTAAGACAGTGGCCAACTGCTGACCGGTGACCAAGCCGACCACTGGCA 219
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 220 GCCGGTATGCTCCACAGCAGAGCCGCTGTGACCCCGCTCTCTGGGCAACCTGTGCTTA 279
QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 280 GGCTTGACACCTTCAAGAGCTGGAGACCACTGGATGGAGATCTCTGGGCGCAGCTGGCG 339
QY 61 ProLeuThrGlnGluGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db 340 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
QY 81 PheProGlyMetGlySerGlyGlnGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db 400 TTCCCGGACATGGGCTGTGAGAGATGCTGTGAGCTGCTGCTCTATGACTGGCCGCTGACT 459
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 460 GCTGAGGTGGCACCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
Db 520 AAGGTGAGTGCTTCTTCTGCTATGGGGGCTGACAGAGCTGAGAGCGGGGAGCAGCCCC 579
QY 141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 580 TGGACGAGATGCAAGTGGTTCCTCCAGCTGTCACTTCTGCTGCTGCTGCTGCTGCTGCTG 639
QY 161 AspPheValHisSerValGlnGlnTyrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 640 GACTTGTCCACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
Db 700 GAAGAACCGGAAACCGAGCCCTGTGGCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
QY 201 LeuProThrProArgArgGluValGlnSerGlnSerAlaGlnGluProGlyAlaArgAsp 220
Db 760 CTCGCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
QY 221 ValGluAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db 820 GTGAGAGCGCAGCTGCGCGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
QY 241 AlaValSerIleValPheValProCysGlyHisIleValCysAlaGluCysAlaProGly 260
Db 880 GCCGTGTCCATGCTCTTGTGTGCGGTGGCCACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
QY 261 LeuGlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
Db 940 CTGCACTGTGCGCCATCTGCAAGAGCCCGCTCCGAGCGCGGTGCGACCTTCTGTGCC 999

```

RESULT 2

US-11-266-748A-23550
Sequence 23550, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harbin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03

```

/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 23550
/ LENGTH: 1260
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-11-266-748A-23550

```

Alignment Scores:

```

Pred. No.: 5,4e-267 Length: 1260
Score: 280.00 Matches: 280
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.6% Indels: 0
DB: 11 Gaps: 0

```

US-09-762-577b-12 (1-309) x US-11-266-748A-23550 (1-1260)

```

QY 1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTyrAla 20
Db 174 ATGGGACCTTAAGACAGTGGCCAACTGCTGACCGGTGACCAAGCCGACCACTGGCA 233
QY 21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db 234 GCCGGTATGCTCCACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 293
QY 41 GlyLeuAspThrCysArgAlaTTPAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db 294 GGCTTGACACCTTCAAGAGCTGGAGACCACTGGATGGAGATCTCTGGGCGCAGCTGGCG 353
QY 61 ProLeuThrGlnGluGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Db 354 CCCCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
QY 81 PheProGlyMetGlySerGlyGlnGluLeuArgLeuAlaSerPheTyrAspTyrProLeuThr 100
Db 414 TTCCCGGACATGGGCTGTGAGAGATGCTGTGAGCTGCTGCTCTATGACTGGCCGCTGACT 473
QY 101 AlaGluValProProGlnLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db 474 GCTGAGGTGGCACCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 121 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTyrLysArgGlyAspAspPro 140
Db 534 AAGGTGAGTGCTTCTTCTGCTATGGGGGCTGACAGAGCTGAGAGCGGGGAGCGAGCCCC 593
QY 141 TyrThrGlnHisAlaLysTyrPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
Db 594 TGGACGAGATGCAAGTGGTTCCTCCAGCTGTCACTTCTGCTGCTGCTGCTGCTGCTGCTG 653
QY 161 AspPheValHisSerValGlnGlnTyrHisSerGlnLeuLeuGlySerTyrAspProTyr 180
Db 654 GACTTGTCCACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
QY 181 GlnGluProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGln 200
Db 714 GAAGAACCGGAAACCGAGCCCTGTGGCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 773

```

Oy	201	LeuPcHtRrProArxArgIValGInsergiUserrAAGInGIUProGIYAlARgsp	220
Dd	774	CTGCCACACCAGAAGAGGTCCAGTGAAGTGCCCAAGACCCAGAACCCAGGGAT	833
Oy	221	VaIGuaIagInLnuArqArgleungIngIUarGrThCySlvseVaICysLeusAsParq	240
Dd	824	GTCGAGCGGCAGCTCGGGCGCTGCAGAGAGAGAGACTGCAAGGTGTGCTGCACCCC	893
Oy	241	AlAVaserIllevalPhelValProcysglYhiSleValCysAlGlucYsaAProGIY	260
Dd	894	GCCGTCATCATCTTTGTGTCCGTGGCCCCCACCTGTGTGTGCTGAGGTGTCGCCCGCG	953
Oy	261	LengInLeuCysPrOILCYsarGaLaPovaLAgsereArgValArgThrphelusier	280
Dd	954	CTGCAGCTGTGCCCATCTGCAGACCCCGTCGCCGAGCGCGGTGGACCTTCTGTTC	1011
 RESULT 3 US-11-266-748A-290500 ; Sequence 290500, Application US/11266748A ; GENERAL INFORMATION: ; APPLICANT: Harkin, Paul ; APPLICANT: Johnston, Patrick ; APPLICANT: Mulligan, Karl ; TITLE OF INVENTION: Transcriptome Microarray Technology and ; FILE REFERENCE: 55815-0102 (319189) ; CURRENT APPLICATION NUMBER: US/11/266,748A ; PRIOR FILING DATE: 2005-11-03 ; PRIOR APPLICATION NUMBER: EP 04105479.2 ; PRIOR FILING DATE: 2004-11-03 ; PRIOR APPLICATION NUMBER: EP 04105482.6 ; PRIOR FILING DATE: 2004-11-03 ; PRIOR APPLICATION NUMBER: EP 04105483.4 ; PRIOR FILING DATE: 2004-11-03 ; PRIOR APPLICATION NUMBER: EP 04105507.0 ; PRIOR FILING DATE: 2004-11-03 ; PRIOR APPLICATION NUMBER: EP 04105485.9 ; PRIOR FILING DATE: 2004-11-03 ; PRIOR APPLICATION NUMBER: EP 04105484.2 ; PRIOR FILING DATE: 2004-11-03 ; PRIOR APPLICATION NUMBER: US 60/662,276 ; PRIOR FILING DATE: 2005-03-14 ; PRIOR APPLICATION NUMBER: US 60/700,293 ; PRIOR FILING DATE: 2005-07-18 ; NUMBER OF SEQ ID NOS: 48396 ; SOFTWARE: PatentIn version 3.3 ; SEQ ID NO 290500 ; LENGTH: 1000 ; TYPE: DNA ; ORGANISM: Homo Sapiens US-11-266-748A-290500			
 Alignment Scores:			
Sred.	No. :	Length:	1000
Score:	248..00	Matches:	248
Percent Similarity:	100..0%	Conservative:	0
Best Local Similarity:	100..0%	Mismatches:	0
Query Match:	80.3%	Indels:	0
DB:	11	Gaps:	0
 US-09-762-577B-12 (1..309) x US-11-266-748A-290500 (1..1000)			
Oy	33	ArgSerLeuglySerProValleuglyLeuasPTThrcysatgaLatrpASPH:IsvAlasp	52
Dd	2	CgccttcTcgGgcaGccctgttctctaaggacctgaacacttgaaagcctggagaccatgatgatt	61
Oy	53	GlyGlnlleuglyGlnLeuarqProleuthrginguinglinguingluyalaglY	72
Dd	62	GggcagaatccTcgGgcCaactCGcgccctGACAAGAgAAAGAGAGAGAGGgCGcCGg	121
Oy	73	AlathrlouserrargglyProialaphetrogilysemGlsueGluGlnLeuarqleuala	92

Db	122	GCCACCTTGTCCAGGGGGGCTGCTTCCCGGCGATGGGCTGTGAGGAGTTGGGCTGGCC	181
Qy	93	SerPheIyTAserTPProleuthrXlaglVal1ProProGluLeuLeuAalAalaglY	112
Db	182	TCCCTCTATGACTGGCCCGCTGACTCTGTGGGGCCACCAGACTGCTGCTGCTGGCC	241
Qy	113	PhePheH1sThrGlyH1sGlnAspIysValaArgCysPhePheCysTyrGlyGlyLeuGln	132
Db	242	TTCTTCCACAGAGGCATCAGACAAAGGTAGAGTGTCTTTCTGTATGAGGGGCTTGACG	301
Qy	133	SetrTlyAsrGlyAAspAspProtrTPThrgluH1sAlaLysTrPheProserCysGln	152
Db	302	AGCTGGAAGCGGGGAGAGACCCCTCGAACGAGCATGCCAAGTGTTCCTCCAGCTTCAG	361
Qy	153	PheLeuLeuAArgSerLeYsGlyAArgAspPheValH1sSerValGlnGluThrH1sSerGln	172
Db	362	TTCCCTGCTCCGGTCAAAAGAGAAAGACTTTGTCCACAGTGTACAGAGACTCCTCCAG	421
Qy	173	LeuLeuGlySerTPAspProtrbgluGluTProGluAspAlaAlaProValAlaProser	192
Db	422	CTGCTGGGCTCTCTGGAGCCCTGGGAGAAAGACCGAAGAGCAGCCCTGTGGCCCTCC	481
Qy	193	ValProAlaSerGlyTYrProGluLeuTProThrProArgArgGluValGlnSerGluSer	212
Db	482	GTCCCTGCTCTGGGTATCTTGAGCTGTGCCACACCCAGAGAGAGGTCCAGTCTGAAAGT	541
Qy	213	AlaGlnGluProGlyAlaArgAspValGluValGlnLeuAArgGluGlnGluArg	232
Db	542	GCCCGAGAGCCAGAGGAGGAGGATGTGGAGGGCGAGCTCGCGGCTGCAGAGGAGAGG	601
Qy	233	ThrCysIysValaCysLeuAspAArgAlaValSerIleValPheValProCysGlyH1sLeu	252
Db	602	ACGTGCAAGGTGTGTCTGTAGCCGCGCGTGTCCATCGTCTTGTGTGGCGGCGCACCTG	661
Qy	253	ValCysAlaGluCysAlaProGlyLeuGlnLeuCysProIleCysAArgAlaProValArg	272
Db	662	GTCTGTGTGTAGTGTGTGGCCCGCGGCTGCAGCTGTGCCCATGTGTGCAGAGCCCCGTCCG	721
Qy	273	SerArgValaArgThrPheLeuSer 280	
Db	722	AGCCGCGTGGCGACCTTCTCTGTCC 745	
RESULT 4			
US-11-266-748A-341929/c			
: Sequence 341929, Application US/11266748A			
: GENERAL INFORMATION:			
: APPLICANT: Hartson, Patrick			
: APPLICANT: Mulligan, Karl			
: TITLE OF INVENTION: Transcriptome Microarray Technology and			
: FILE REFERENCE: 55815-0102 (319189)			
: CURRENT FILING DATE: US/11/266,748A			
: PRIOR FILING DATE: 2005-11-03			
: PRIOR FILING DATE: 2004-11-03			
: PRIOR FILING DATE: 2004-11-03			
: PRIOR FILING DATE: 2004-11-03			
: PRIOR FILING DATE: 2004-11-03			
: PRIOR FILING DATE: 2004-11-03			
: PRIOR FILING DATE: 2004-11-03			
: PRIOR FILING DATE: 2005-03-14			
: PRIOR FILING DATE: 2005-07-18			
: NUMBER OF SEQ ID NOS: 48396			
: SOFTWARE: PatentIn version 3.3			
: SEQ ID NO 341929			

```

; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-341929

Alignment Scores:
Pred. No.: 2,2e-235      Length: 1000
Score: 248.00           Matches: 248
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match: 80.3%        Indels: 0
DB: 11                   Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-341929 (1-1000)

QY 33  ArgSerLeuGlySerProValLeuGlyLeuAspThrCysArgAlaTAPAspHisValAsp 52
DB 999  CGCTCTCGGGAGAGCCCTGCTCTAGGCGCTTGACACCTGACAGAGCTGGAGCCAGCTGGAT 940
QY 53  GlyGlnIleLeuGlyGlnLeuArgProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGln 72
DB 939  GGGAGAGATCTCTGGGCGAGCTCGGCGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAG 880
QY 73  AlaThrLeuSerArgGlyProAlaPheProGlyMetGlySerGlnGlnLeuArgLeuAla 92
DB 879  GCCACCTTGTCAGAGGGGCGCTGCTCCCGGCATGGGCTCTGAGAGAGTTGGCTCTGGCC 820
QY 93  SerPheTyrAspTTPProLeuThrAlaGlnValProProGlnLeuLeuAlaAlaGly 112
DB 819  TCCTTCTATGACTGGCGCGCTGACTGCTGAGGTGCACCCAGAGCTGCTGCTGCTGCGCGC 760
QY 113  PhePheHisThrGlyHisGlnAspLysValArgCysPhePheCysTyrGlyGlyLeuGln 132
DB 759  TTCTTCCACACAGCGCCATCAGAGCAAGGTAGGCTTCTTCTGCTATGGGGGCTTGCAG 700
QY 133  SerTyrLysArgGlyAspAspProTyrThrGlnHisAlaLysTyrPheProSerCysGln 152
DB 699  AGCTGGAAAGCGGGGAGAGCCCTGAGCAGAGACATGCCAAGGTGTTCCCGCAGCTGTGAG 640
QY 153  PheLeuLeuArgSerLysGlyArgAspPheValHisSerValGlnGlnThrHisSerGln 172
DB 639  TTCTGCTCCGGTCMAAAGAGAGACTTGTGCACAGTGTGAGAGAGACTGCTCCAG 580
QY 173  LeuLeuGlnSerTyrPAPProTyrProGlnGlnProGlnAspAlaAlaProValAlaProSer 192
DB 579  CTGCTGGGCTCTCTGGGAGCCCGGTGGAAAGACCGAAGACGAGCCCTGTGGCGCCCTCC 520
QY 193  ValProAlaSerGlyTyrProGlnLeuProThrProArgArgGlnValGlnSerGlnUser 212
DB 519  GTCCCTGCTCTGGGTACCTGTAGCTGCCACACCCAGAGAGAGAGTCCAGTCTGAAAGT 460
QY 213  AlaGlnGlnProGlyAlaArgAspValGlnAlaGlnLeuArgArgLeuGlnGlnGlnGln 232
DB 459  GCCCAGAGAGCCAGAGCCAGAGGTGAGAGCGCAGCTCGCGCGCTGAGAGAGAGAGAGG 400
QY 233  ThrCysLeuValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeu 252
DB 399  ACCTGCAAGGTGTGCTTGAACCGCGCGCTGCTCATGTCTTGTGCTCGGTGGCCACCTG 340
QY 253  ValCysAlaGlnCysAlaProGlyLeuGlnLeuCysProIleCysArgAlaProValArg 272
DB 339  GTCTGTGTGAGAGTGTCCCGCGCTGAGAGCTGTGCCCATGTGACAGAGCCCGGTCCGC 280
QY 273  SerArgValArgThrPheLeuSer 280
DB 279  AGCCGCGTGGCAGCTTCTGTGCTC 256

RESULT 5
US-11-266-748A-211754/c
; Sequence 211754, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Johnston, Patrick
```

```

; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent version 3.3
; SEQ ID NO 211754
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-211754

Alignment Scores:
Pred. No.: 9.15e-108      Length: 633
Score: 119.00           Matches: 119
Percent Similarity: 100.0%  Conservative: 0
Best Local Similarity: 100.0%  Mismatches: 0
Query Match: 38.5%        Indels: 0
DB: 11                   Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-211754 (1-633)

QY 162  PheValHisSerValGlnGlnThrHisSerGlnLeuLeuGlySerTyrAspProTyrGln 181
DB 622  TTGTCCACAGTGTGAGAGAGACTCACTCCAGACTGTGGCTTTGGAGCCGTGGAGAA 563
QY 182  GlnProGlnAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlnLeu 201
DB 562  GAACCGGAAACCCAGAGCCCTGTGGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503
QY 202  ProThrProArgArgGlnValGlnSerGlnUserAlaGlnGlnProGlyAlaArgAspVal 221
DB 502  CCCACACCCAGAGAGAGAGTCCAGTCTGAAAGTCCCAAGAGCCAGAGAGCCAGAGATGTG 443
QY 222  GlnAlaGlnLeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 241
DB 442  GAGCGCCAGCTGGCGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
QY 242  ValSerIleValPheValProCysGlyHisLeuValCysAlaGlnCysAlaProGlyLeu 261
DB 382  GTTCTCATGTCTTGTGCGGTGCGGCGCCCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 323
QY 262  GlnLeuCysProIleCysArgAlaProValAlaSerArgValArgThrPheLeuSer 280
DB 322  CAGCTGTGCCCATCTGACAGAGCCCGGTCCGACCGCGTGGCAGCCTTCTGTCTC 266

RESULT 6
US-11-266-748A-235360
; Sequence 235360, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
```

```
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 235360
LENGTH: 633
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-235360

Alignment Scores:
Pred. No.: 9,15e-108      Length: 633
Score: 119.00           Matches: 119
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 38.5%             Indels: 0
DB: 11                       Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-235360 (1-633)

Qy 162 PheValHisSerValGlnGlnThiHisSerGlnLeuGlySerTyrPAspProTyrGlu 181
    |||||
Db 12 TTGTCCACAGTGTGCAGAGACTCCTCCAGCTGCTGGGCTTGGGACCCCTGGGAA 71

Qy 182 GluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGluLeu 201
    |||||
Db 72 GAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 131

Qy 202 ProThrProArgArgGlnValGlnSerGlnSerAlaGlnGlnGluProGlyAlaArgAspVal 221
    |||||
Db 132 CCCACACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191

Qy 222 GluAlaGlnLeuArgArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 241
    |||||
Db 192 GAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251

Qy 242 ValSerIleValPheValProCysGlyHisLeuValCysAlaGluCysAlaProGlyLeu 261
    |||||
Db 252 GTGTCATCGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311

Qy 262 GlnLeuCysProIleCysArgAlaProValArgSerArgValArgThrPheLeuSer 280
    |||||
Db 312 CAGCTGAGCCCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368

RESULT 7
US-09-762-577B-49
Sequence 49, Application US/09762577B
GENERAL INFORMATION:
APPLICANT: Dranooff, Glenn
APPLICANT: Schmollinger, Jan
APPLICANT: Hodi, F. Stephen
APPLICANT: Molllick, Joseph
TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
FILE REFERENCE: 2486/109
CURRENT APPLICATION NUMBER: US/09/762,577B
CURRENT FILING DATE: 2002-08-29
```

```
PRIOR APPLICATION NUMBER: 60/095,766
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 226
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 163..168
OTHER INFORMATION: n = A,T,C or G
US-09-762-577B-49

Alignment Scores:
Pred. No.: 4,09e-08      Length: 226
Score: 18.00           Matches: 18
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 5.8%             Indels: 0
DB: 5                       Gaps: 0

US-09-762-577B-12 (1-309) x US-09-762-577B-49 (1-226)

Qy 1 MetGlyProIysAspSerAlaIleValCysLeuHisArgGlyProGlnProSerHis 18
    |||||
Db 172 ATGGAGCTTAAGACAGTGTCCAGTGTCTACCGTGAGACACAGCGGAGCCGAC 225

RESULT 8
US-11-266-748A-41998
Sequence 41998, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 41998
LENGTH: 634
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-41998

Alignment Scores:
Pred. No.: 0.00097      Length: 634
Score: 14.00           Matches: 14
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match: 4.5%             Indels: 0
DB: 11                       Gaps: 0

US-09-762-577B-12 (1-309) x US-11-266-748A-41998 (1-634)
```

QY 224 GlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCys 237
|||||
DB 88 CAATTGAGAGGTTGCAGAGAGAACTGTAAAGTGTCT 129
RESULT 9
US-11-266-748A-15520
; Sequence 15520, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15520
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (641)..(696)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (712)..(712)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (800)..(800)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (873)..(873)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (887)..(887)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-15520
Alignment Scores:
Pred. No.: 0.00138 Length: 927
Score: 14.00 Matches: 14
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
DB: 11 Gaps: 0
US-09-762-577B-12 (1-309) x US-11-266-748A-15520 (1-927)
QY 224 GlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCys 237
|||||
DB 224 GlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCys 237
|||||

DB 78 CAATTGCGAGACTACAGAGAGAAACATGTAAAGTGTCT 119
RESULT 10
US-11-266-748A-21170
; Sequence 21170, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21170
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (641)..(696)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (712)..(712)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (800)..(800)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (873)..(873)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (887)..(887)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-21170
Alignment Scores:
Pred. No.: 0.00138 Length: 927
Score: 14.00 Matches: 14
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
DB: 11 Gaps: 0
US-09-762-577B-12 (1-309) x US-11-266-748A-21170 (1-927)
QY 224 GlnLeuArgArgLeuGlnGlnGluArgThrCysLysValCys 237
|||||
DB 78 CAATTGCGAGACTACAGAGAGAAACATGTAAAGTGTCT 119
RESULT 11


```
US-11-266-748A-13769
; Sequence 13769, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; ORGANISM: Homo Sapiens
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-13769

Alignment Scores:
Pred. No.: 0.00139 Length: 934
Score: 14.00 Matches: 14
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
Gaps: 0
DB: 11

US-09-762-577B-12 (1-309) x US-11-266-748A-13769 (1-934)
Qy 224 GlnleuArGArGleuGlnGluArGThrCysIysValCys 237
Db 277 CAATTGAGAGGTTGCAAGAGAACGAACTTGTAAGTGCT 318

RESULT 12
US-11-266-748A-115538
; Sequence 115538, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; ORGANISM: Homo Sapiens
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-157702

Alignment Scores:
Pred. No.: 0.00148 Length: 1000
Score: 14.00 Matches: 14
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
Gaps: 0
DB: 11

US-09-762-577B-12 (1-309) x US-11-266-748A-157702 (1-1000)
Qy 224 GlnleuArGArGleuGlnGluArGThrCysIysValCys 237
Db 327 CAATTGAGAGGTTGCAAGAGAACGAACTTGTAAGTGCT 368

RESULT 13
US-11-266-748A-157702/c
; Sequence 157702, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; ORGANISM: Homo Sapiens
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-157702

Alignment Scores:
Pred. No.: 0.00148 Length: 1000
Score: 14.00 Matches: 14
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.5% Indels: 0
Gaps: 0
DB: 11

US-09-762-577B-12 (1-309) x US-11-266-748A-157702 (1-1000)
Qy 224 GlnleuArGArGleuGlnGluArGThrCysIysValCys 237
```

Db 674 CAATTGAGAGTTCACAGAAACGACCTGTAAAGTGT 633

RESULT 14

US-11-266-748A-220957

Sequence 220957, Application US/11266748A

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Patrick

TITLE OF INVENTION: Transcriptome Microarray Technology and

FILE REFERENCE: 55815-0102 (319189)

CURRENT FILING DATE: 2005-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03